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(54) Title: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS FOR THEIR USE

## (57) Abstract

Compounds and methods for diagnosing prostate cancer are provided. The inventive compounds include polypeptides containing at least a portion of a prostate tumor protein. The inventive polypeptides may be used to generate antibodies useful for the diagnosis and monitoring of prostate cancer. Nucleic acid sequences for preparing probes, primers, and polypeptides are also provided.

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## COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS FOR THEIR USE

### TECHNICAL FIELD

The present invention relates generally to the treatment and monitoring of prostate cancer. The invention is more particularly related to polypeptides comprising at least a portion of a prostate protein. Such polypeptides may be used for the production of compounds, such as antibodies, useful for diagnosing and monitoring the progression of prostate cancer, and possibly other tumor types, in a patient.

### BACKGROUND OF THE INVENTION

Prostate cancer is the most common form of cancer among males, with an estimated incidence of 30% in men over the age of 50. Overwhelming clinical evidence shows that human prostate cancer has the propensity to metastasize to bone, and the disease appears to progress inevitably from androgen dependent to androgen refractory status, leading to increased patient mortality. This prevalent disease is currently the second leading cause of cancer death among men in the U.S.

In spite of considerable research into diagnosis and therapy of the disease, prostate cancer remains difficult to detect and to treat. Commonly, treatment is based on surgery and/or radiation therapy, but these methods are ineffective in a significant percentage of cases. Two previously identified prostate specific proteins - prostate specific antigen (PSA) and prostatic acid phosphatase (PAP) - have limited diagnostic and therapeutic potential. For example, PSA levels do not always correlate well with the presence of prostate cancer, being positive in a percentage of non-prostate cancer cases, including benign prostatic hyperplasia (BPH). Furthermore, PSA measurements correlate with prostate volume, and do not indicate the level of metastasis.

Accordingly, there remains a need in the art for improved and diagnostic methods for prostate cancer.

## SUMMARY OF THE INVENTION

The present invention provides methods for immunodiagnosis of prostate cancer, together with kits for use in such methods. Polypeptides are disclosed which comprise at least an immunogenic portion of a prostate tumor protein or a variant of said protein that differs only in conservative substitutions and/or modifications, wherein the prostate tumor protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-11, 115-171, 173-175, 177, 179-224 and variants thereof. Such polypeptides may be usefully employed in the diagnosis and monitoring of prostate cancer.

In one specific aspect of the present invention, methods are provided for detecting prostate cancer in a patient, comprising: (a) contacting a biological sample obtained from a patient with a binding agent that is capable of binding to one of the above polypeptides; and (b) detecting in the sample a protein or polypeptide that binds to the binding agent. In preferred embodiments, the binding agent is an antibody, most preferably a monoclonal antibody.

In related aspects, methods are provided for monitoring the progression of prostate cancer in a patient, comprising: (a) contacting a biological sample obtained from a patient with a binding agent that is capable of binding to one of the above polypeptides; (b) determining in the sample an amount of a protein or polypeptide that binds to the binding agent; (c) repeating steps (a) and (b); and comparing the amounts of polypeptide detected in steps (b) and (c).

Within related aspects, the present invention provides antibodies, preferably monoclonal antibodies, that bind to the inventive polypeptides, as well as diagnostic kits comprising such antibodies, and methods of using such antibodies to inhibit the development of prostate cancer.

The present invention further provides methods for detecting prostate cancer comprising: (a) obtaining a biological sample from a patient; (b) contacting the sample with a first and a second oligonucleotide primer in a polymerase chain reaction, at least one of the oligonucleotide primers being specific for a DNA molecule that encodes one of the above polypeptides; and (c) detecting in the sample a DNA sequence that amplifies in the presence of the first and second oligonucleotide primers. In a preferred embodiment, at least one of the

generate antibodies that detect the presence or absence of prostate cancer. Such modified sequences may be prepared and tested using, for example, the representative procedures described herein.

As used herein, a "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydropathic nature of the polypeptide to be substantially unchanged. In general, the following groups of amino acids represent conservative changes: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his.

Variants may also, or alternatively, contain other modifications, including the deletion or addition of amino acids that have minimal influence on the antigenic properties, secondary structure and hydropathic nature of the polypeptide. For example, a polypeptide may be conjugated to a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (e.g., poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

A nucleotide "variant" is a sequence that differs from the recited nucleotide sequence in having one or more nucleotide deletions, substitutions or additions. Such modifications may be readily introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis as taught, for example, by Adelman et al. (DNA, 2:183, 1983). Nucleotide variants may be naturally occurring allelic variants, or non-naturally occurring variants. Variant nucleotide sequences preferably exhibit at least about 70%, more preferably at least about 80% and most preferably at least about 90% identity to the recited sequence. Such variant nucleotide sequences will generally hybridize to the recited nucleotide sequence under stringent conditions. As used herein, "stringent conditions" refers to prewashing in a solution of 6X SSC, 0.2% SDS; hybridizing at 65 °C, 6X SSC, 0.2% SDS overnight; followed by two washes of 30 minutes each in 1X SSC, 0.1% SDS at 65 °C and two washes of 30 minutes each in 0.2X SSC, 0.1% SDS at 65 °C.

"Polypeptides" as used herein also include combination, or fusion, polypeptides. A "combination polypeptide" is a polypeptide comprising at least one of the above immunogenic portions and one or more additional immunogenic prostate tumor-specific sequences, which are joined via a peptide linkage into a single amino acid chain. The sequences may be joined directly (*i.e.*, with no intervening amino acids) or may be joined by way of a linked sequence (*e.g.*, Gly-Cys-Gly) that does not significantly diminish the immunogenic properties of the component polypeptides.

The prostate tumor proteins of the present invention, and DNA molecules encoding such proteins, may be isolated from prostate tumor tissue using any of a variety of methods well known in the art. DNA sequences corresponding to a gene (of a portion thereof) encoding one of the inventive prostate tumor proteins may be isolated from a prostate tumor cDNA library using a subtraction technique as described in detail below. Examples of such DNA sequences are provided in SEQ ID Nos: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Partial DNA sequences thus obtained may be used to design oligonucleotide primers for the amplification of full-length DNA sequences in a polymerase chain reaction (PCR), using techniques well known in the art (see, for example, Mullis et al., *Cold Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich ed., *PCR Technology*, Stockton Press, NY, 1989). Once a DNA sequence encoding a polypeptide is obtained, any of the above modifications may be readily introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis as taught, for example, by Adelman et al. (*DNA*, 2:183, 1983).

The prostate tumor polypeptides disclosed herein may also be generated by synthetic or recombinant means. Synthetic polypeptides having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may be generated using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain (see, for example, Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963). Equipment for automated synthesis of polypeptides is commercially available from

oligonucleotide primers comprises at least about 10 contiguous nucleotides of a DNA molecule having a partial sequence selected from the group consisting of SEQ ID Nos: 2-3, 5-107, 109-11, 115-171, 173-175, 177 and 179-224.

In a further aspect, the present invention provides a method for detecting prostate cancer in a patient comprising: (a) obtaining a biological sample from the patient; (b) contacting the sample with an oligonucleotide probe specific for a DNA molecule that encodes one of the above polypeptides; and (c) detecting in the sample a DNA sequence that hybridizes to the oligonucleotide probe. Preferably, the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA molecule having a partial sequence selected from the group consisting of SEQ ID Nos: 2-3, 5-107, 109-11, 115-171, 173-175, 177 and 179-224.

In related aspects, diagnostic kits comprising the above oligonucleotide probes or primers are provided.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

#### DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to compositions and methods for the immunodiagnosis and monitoring of prostate cancer. The inventive compositions are generally polypeptides that comprise at least a portion of a prostate tumor protein. Also included within the present invention are molecules (such as an antibody or fragment thereof) that bind to the inventive polypeptides. Such molecules are referred to herein as "binding agents."

In particular, the subject invention discloses polypeptides comprising at least a portion of a human prostate tumor protein, or a variant thereof such a protein, wherein the prostate tumor protein includes an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-11, 115-171, 173-175, 177, 179-224, the complements of said nucleotide sequences and variants thereof. As used herein, the term "polypeptide"

encompasses amino acid chains of any length, including full length proteins, wherein the amino acid residues are linked by covalent peptide bonds. Thus, a polypeptide comprising a portion of one of the above prostate proteins may consist entirely of the portion, or the portion may be present within a larger polypeptide that contains additional sequences. The additional sequences may be derived from the native protein or may be heterologous, and such sequences may be immunoreactive and/or antigenic.

As used herein, an "immunogenic portion" of a human prostate tumor protein is a portion that is capable of eliciting an immune response in a patient inflicted with prostate cancer and as such binds to antibodies present within sera from a prostate cancer patient. Immunogenic portions of the proteins described herein may thus be identified in antibody binding assays. Such assays may generally be performed using any of a variety of means known to those of ordinary skill in the art, as described, for example, in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 1988. For example, a polypeptide may be immobilized on a solid support (as described below) and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example, <sup>125</sup>I-labeled Protein A. Alternatively, a polypeptide may be used to generate monoclonal and polyclonal antibodies for use in detection of the polypeptide in blood or other fluids of prostate cancer patients.

The compositions and methods of the present invention also encompass variants of the above polypeptides and DNA molecules. A polypeptide "variant," as used herein, is a polypeptide that differs from the recited polypeptide only in conservative substitutions and/or modifications, such that the therapeutic, antigenic and/or immunogenic properties of the polypeptide are retained. Polypeptide variants preferably exhibit at least about 70%, more preferably at least about 90% and most preferably at least about 95% identity to the identified polypeptides. For prostate tumor polypeptides with immunoreactive properties, variants may, alternatively, be identified by modifying the amino acid sequence of one of the above polypeptides, and evaluating the immunoreactivity of the modified polypeptide. For prostate tumor polypeptides useful for the generation of diagnostic binding agents, a variant may be identified by evaluating a modified polypeptide for the ability to

suppliers such as Perkin Elmer/Applied BioSystems Division (Foster City, CA), and may be operated according to the manufacturer's instructions.

Alternatively, any of the above polypeptides may be produced recombinantly by inserting a DNA sequence that encodes the polypeptide into an expression vector and expressing the protein in an appropriate host. Any of a variety of expression vectors known to those of ordinary skill in the art may be employed to express recombinant polypeptides of this invention. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast and higher eukaryotic cells. Preferably, the host cells employed are *E. coli*, yeast or a mammalian cell line, such as CHO cells. The DNA sequences expressed in this manner may encode naturally occurring polypeptides, portions of naturally occurring polypeptides, or other variants thereof.

In general, regardless of the method of preparation, the polypeptides disclosed herein are prepared in substantially pure form (*i.e.*, the polypeptides are homogenous as determined by amino acid composition and primary sequence analysis). Preferably, the polypeptides are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure. In certain embodiments, described in more detail below, the substantially pure polypeptides are incorporated into pharmaceutical compositions or vaccines for use in one or more of the methods disclosed herein.

In a related aspect, the present invention provides fusion proteins comprising a first and a second inventive polypeptide or, alternatively, a polypeptide of the present invention and a known prostate antigen, together with variants of such fusion proteins. The fusion proteins of the present invention may also include a linker peptide between the first and second polypeptides.

A DNA sequence encoding a fusion protein of the present invention is constructed using known recombinant DNA techniques to assemble separate DNA sequences encoding the first and second polypeptides into an appropriate expression vector. The 3' end of a DNA sequence encoding the first polypeptide is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide so that the reading frames

of the sequences are in phase to permit mRNA translation of the two DNA sequences into a single fusion protein that retains the biological activity of both the first and the second polypeptides.

A peptide linker sequence may be employed to separate the first and the second polypeptides by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al., *Proc. Natl. Acad. Sci. USA* 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may be from 1 to about 50 amino acids in length. Peptide sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons required to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

Polypeptides and/or fusion proteins of the present invention may be used to generate binding agents, such as antibodies or fragments thereof, that are capable of detecting metastatic human prostate tumors. Binding agents of the present invention may generally be prepared using methods known to those of ordinary skill in the art, including the representative procedures described herein. Binding agents are capable of differentiating between patients with and without prostate cancer, using the representative assays described

herein. In other words, antibodies or other binding agents raised against a prostate tumor protein, or a suitable portion thereof, will generate a signal indicating the presence of primary or metastatic prostate cancer in at least about 20% of patients afflicted with the disease, and will generate a negative signal indicating the absence of the disease in at least about 90% of individuals without primary or metastatic prostate cancer. Suitable portions of such prostate tumor proteins are portions that are able to generate a binding agent that indicates the presence of primary or metastatic prostate cancer in substantially all (*i.e.*, at least about 80%, and preferably at least about 90%) of the patients for which prostate cancer would be indicated using the full length protein, and that indicate the absence of prostate cancer in substantially all of those samples that would be negative when tested with full length protein. The representative assays described below, such as the two-antibody sandwich assay, may generally be employed for evaluating the ability of a binding agent to detect metastatic human prostate tumors.

The ability of a polypeptide and/or fusion protein prepared as described herein to generate antibodies capable of detecting primary or metastatic human prostate tumors may generally be evaluated by raising one or more antibodies against the polypeptide (using, for example, a representative method described herein) and determining the ability of such antibodies to detect such tumors in patients. This determination may be made by assaying biological samples from patients with and without primary or metastatic prostate cancer for the presence of a polypeptide that binds to the generated antibodies. Such test assays may be performed, for example, using a representative procedure described below. Polypeptides that generate antibodies capable of detecting at least 20% of primary or metastatic prostate tumors by such procedures are considered to be useful in assays for detecting primary or metastatic human prostate tumors. Polypeptide specific antibodies may be used alone or in combination to improve sensitivity.

Polypeptides and/or fusion proteins capable of detecting primary or metastatic human prostate tumors may be used as markers for diagnosing prostate cancer or for monitoring disease progression in patients. In one embodiment, prostate cancer in a patient may be diagnosed by evaluating a biological sample obtained from the patient for the level of

one or more of the above polypeptides, relative to a predetermined cut-off value. As used herein, suitable "biological samples" include blood, sera, urine and/or prostate secretions.

The level of one or more of the above polypeptides may be evaluated using any binding agent specific for the polypeptide(s). A "binding agent," in the context of this invention, is any agent (such as a compound or a cell) that binds to a polypeptide as described above. As used herein, "binding" refers to a noncovalent association between two separate molecules (each of which may be free (*i.e.*, in solution) or present on the surface of a cell or a solid support), such that a "complex" is formed. Such a complex may be free or immobilized (either covalently or noncovalently) on a support material. The ability to bind may generally be evaluated by determining a binding constant for the formation of the complex. The binding constant is the value obtained when the concentration of the complex is divided by the product of the component concentrations. In general, two compounds are said to "bind" in the context of the present invention when the binding constant for complex formation exceeds about  $10^3$  L/mol. The binding constant may be determined using methods well known to those of ordinary skill in the art.

Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome with or without a peptide component, an RNA molecule or a peptide. In a preferred embodiment, the binding partner is an antibody, or a fragment thereof. Such antibodies may be polyclonal, or monoclonal. In addition, the antibodies may be single chain, chimeric, CDR-grafted or humanized. Antibodies may be prepared by the methods described herein and by other methods well known to those of skill in the art.

There are a variety of assay formats known to those of ordinary skill in the art for using a binding partner to detect polypeptide markers in a sample. *See, e.g.*, Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In a preferred embodiment, the assay involves the use of binding partner immobilized on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a second binding partner that contains a reporter group. Suitable second binding partners include antibodies that bind to the binding partner/polypeptide complex. Alternatively, a competitive assay may be utilized, in which a

polypeptide is labeled with a reporter group and allowed to bind to the immobilized binding partner after incubation of the binding partner with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding partner is indicative of the reactivity of the sample with the immobilized binding partner.

The solid support may be any material known to those of ordinary skill in the art to which the antigen may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the antigen and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the binding agent, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of binding agent ranging from about 10 ng to about 10  $\mu$ g, and preferably about 100 ng to about 1  $\mu$ g, is sufficient to immobilize an adequate amount of binding agent.

Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the binding agent may be covalently attached to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (see, e.g., Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is a two-antibody sandwich assay. This assay may be performed by first contacting an antibody that has been immobilized on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a second antibody (containing a reporter group) capable of binding to a different site on the polypeptide is added. The amount of second antibody that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20<sup>TM</sup> (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.*, incubation time) is that period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with prostate cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20<sup>TM</sup>. The second antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include enzymes (such as horseradish peroxidase), substrates, cofactors, inhibitors, dyes, radionuclides, luminescent groups, fluorescent groups and biotin. The conjugation of antibody to reporter group may be achieved using standard methods known to those of ordinary skill in the art.

The second antibody is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a period of time. Unbound second antibody is then removed and bound second antibody is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of prostate cancer, the signal detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value is the average mean signal obtained when the immobilized antibody is incubated with samples from patients without prostate cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for prostate cancer. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985, p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (*i.e.*, sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for prostate cancer.

In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the antibody is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized antibody as the sample passes through the membrane. A second, labeled antibody then binds to the antibody-polypeptide complex as a solution containing the second antibody flows through the membrane. The detection of bound second antibody may then be performed as described above. In the strip test format, one end of the membrane to which antibody is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second antibody and to the area of immobilized antibody. Concentration of second antibody at the area of immobilized antibody indicates the presence of prostate cancer. Typically, the concentration of second antibody at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of antibody immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in the format discussed above. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1 $\mu$ g, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological sample.

Of course, numerous other assay protocols exist that are suitable for use with the antigens or antibodies of the present invention. The above descriptions are intended to be exemplary only.

In another embodiment, the above polypeptides may be used as markers for the progression of prostate cancer. In this embodiment, assays as described above for the diagnosis of prostate cancer may be performed over time, and the change in the level of reactive polypeptide(s) evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter performed as needed. In general, prostate cancer is progressing in those patients in whom the level of polypeptide detected by the binding agent increases over time. In contrast, prostate cancer is not progressing when the level of reactive polypeptide either remains constant or decreases with time.

Antibodies for use in the above methods may be prepared by any of a variety of techniques known to those of ordinary skill in the art. *See, e.g.*, Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In one such technique, an immunogen comprising the antigenic polypeptide is initially injected into any of a wide variety of mammals (*e.g.*, mice, rats, rabbits, sheep and goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for the antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (*i.e.*, reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield,

such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

Monoclonal antibodies of the present invention may also be used as therapeutic reagents, to diminish or eliminate prostate tumors. The antibodies may be used on their own (for instance, to inhibit metastases) or coupled to one or more therapeutic agents. Suitable agents in this regard include radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include  $^{90}\text{Y}$ ,  $^{123}\text{I}$ ,  $^{125}\text{I}$ ,  $^{131}\text{I}$ ,  $^{186}\text{Re}$ ,  $^{188}\text{Re}$ ,  $^{211}\text{At}$ , and  $^{212}\text{Bi}$ . Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diphtheria toxin, cholera toxin, gelonin, *Pseudomonas* exotoxin, *Shigella* toxin, and pokeweed antiviral protein.

A therapeutic agent may be coupled (e.g., covalently bonded) to a suitable monoclonal antibody either directly or indirectly (e.g., via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulfhydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (e.g., a halide) on the other.

Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the

catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulfhydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, *e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.

Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (*e.g.*, U.S. Patent No. 4,489,710, to Spitler), by irradiation of a photolabile bond (*e.g.*, U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of derivatized amino acid side chains (*e.g.*, U.S. Patent No. 4,638,045, to Kohn et al.), by serum complement-mediated hydrolysis (*e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (*e.g.*, U.S. Patent No. 4,569,789, to Blattler et al.).

It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or linkers which provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (*e.g.*, U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (*e.g.*, U.S. Patent No. 4,699,784, to Shih et al.). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (*e.g.*, U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating compounds that include those containing

nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

A variety of routes of administration for the antibodies and immunoconjugates may be used. Typically, administration will be intravenous, intramuscular, subcutaneous or in the bed of a resected tumor. It will be evident that the precise dose of the antibody/immunoconjugate will vary depending upon the antibody used, the antigen density on the tumor, and the rate of clearance of the antibody.

Diagnostic reagents of the present invention may also comprise DNA sequences encoding one or more of the above polypeptides, or one or more portions thereof. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify prostate tumor-specific cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for a DNA molecule encoding a prostate tumor protein of the present invention. The presence of the amplified cDNA is then detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes specific for a DNA molecule encoding a prostate tumor protein of the present invention may be used in a hybridization assay to detect the presence of an inventive polypeptide in a biological sample.

As used herein, the term "oligonucleotide primer/probe specific for a DNA molecule" means an oligonucleotide sequence that has at least about 80%, preferably at least about 90% and more preferably at least about 95%, identity to the DNA molecule in question. Oligonucleotide primers and/or probes which may be usefully employed in the inventive diagnostic methods preferably have at least about 10-40 nucleotides. In a preferred embodiment, the oligonucleotide primers comprise at least about 10 contiguous nucleotides of a DNA molecule having a sequence selected from SEQ ID Nos: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Preferably, oligonucleotide probes for use in the inventive diagnostic methods comprise at least about 15 contiguous oligonucleotides of a DNA molecule having a sequence provided in SEQ ID Nos: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Techniques for both PCR based assays and hybridization assays are well known in the art (see, for example, Mullis et al. *Ibid*; Ehrlich, *Ibid*). Primers or probes may

thus be used to detect prostate tumor-specific sequences in biological samples, including blood, semen, prostate tissue and/or prostate tumor tissue.

Polypeptides of the present invention that comprise an immunogenic portion of a prostate tumor protein may also be used for immunotherapy of prostate cancer, wherein the polypeptide stimulates the patient's own immune response to prostate tumor cells. In further aspects, the present invention provides methods for using one or more of the immunoreactive polypeptides encoded by a DNA molecule having a sequence provided in SEQ ID NO: 1-107, 109-111, 115-171, 173-175, 177 and 179-224 (or DNA encoding such polypeptides) for immunotherapy of prostate cancer in a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may be afflicted with a disease, or may be free of detectable disease. Accordingly, the above immunoreactive polypeptides may be used to treat prostate cancer or to inhibit the development of prostate cancer. The polypeptides may be administered either prior to or following surgical removal of primary tumors and/or treatment by administration of radiotherapy and conventional chemotherapeutic drugs.

In these aspects, the polypeptide is generally present within a pharmaceutical composition and/or a vaccine. Pharmaceutical compositions may comprise one or more polypeptides, each of which may contain one or more of the above sequences (or variants thereof), and a physiologically acceptable carrier. The vaccines may comprise one or more of such polypeptides and a non-specific immune response enhancer, such as an adjuvant, biodegradable microsphere (e.g., polylactic galactide) or a liposome (into which the polypeptide is incorporated). Pharmaceutical compositions and vaccines may also contain other epitopes of prostate tumor antigens, either incorporated into a combination polypeptide (i.e., a single polypeptide that contains multiple epitopes) or present within a separate polypeptide.

Alternatively, a pharmaceutical composition or vaccine may contain DNA encoding one or more of the above polypeptides, such that the polypeptide is generated *in situ*. In such pharmaceutical compositions and vaccines, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacteria and viral expression systems. Appropriate nucleic acid

expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an epitope of a prostate cell antigen on its cell surface. In a preferred embodiment, the DNA may be introduced using a viral expression system (e.g., vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic (defective), replication competent virus. Suitable systems are disclosed, for example, in Fisher-Hoch et al., *PNAS* 86:317-321, 1989; Flexner et al., *Ann. N.Y. Acad. Sci.* 569:86-103, 1989; Flexner et al., *Vaccine* 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner, *Biotechniques* 6:616-627, 1988; Rosenfeld et al., *Science* 252:431-434, 1991; Kolls et al., *PNAS* 91:215-219, 1994; Kass-Eisler et al., *PNAS* 90:11498-11502, 1993; Guzman et al., *Circulation* 88:2838-2848, 1993; and Guzman et al., *Cir. Res.* 73:1202-1207, 1993. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described, for example, in published PCT application WO 90/11092, and Ulmer et al., *Science* 259:1745-1749, 1993, reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

Routes and frequency of administration, as well as dosage, will vary from individual to individual and may parallel those currently being used in immunotherapy of other diseases. In general, the pharmaceutical compositions and vaccines may be administered by injection (e.g., intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (e.g., by aspiration) or orally. Between 1 and 10 doses may be administered over a 3-24 week period. Preferably, 4 doses are administered, at an interval of 3 months, and booster administrations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of polypeptide or DNA that is effective to raise an immune response (cellular and/or humoral) against prostate tumor cells in a treated patient. A suitable immune response is at least 10-50% above the basal (i.e., untreated) level. In general, the amount of polypeptide present in a dose (or produced *in situ* by the DNA in a dose) ranges from about 1 pg to about 100 mg per kg of host, typically from

about 10 pg to about 1 mg, and preferably from about 100 pg to about 1  $\mu$ g. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.01 mL to about 5 mL.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary depending on the mode of administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a lipid, a wax and/or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and/or magnesium carbonate, may be employed. Biodegradable microspheres (e.g., polylactic glycolide) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Any of a variety of non-specific immune response enhancers may be employed in the vaccines of this invention. For example, an adjuvant may be included. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a nonspecific stimulator of immune response, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis*. Such adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI) and Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ).

Polypeptides disclosed herein may also be employed in *ex vivo* treatment of prostate cancer. For example, cells of the immune system, such as T cells, may be isolated from the peripheral blood of a patient, using a commercially available cell separation system, such as CellPro Incorporated's (Bothell, WA) CEPRATE™ system (see U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). The separated cells are stimulated with one or more of the immunoreactive polypeptides contained within a delivery vehicle, such as a microsphere, to provide antigen-specific T cells. The population of tumor antigen-specific T cells is then expanded using standard techniques and the cells are administered back to the patient.

The following Examples are offered by way of illustration and not by way of limitation.

### EXAMPLES

#### EXAMPLE 1

##### ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES

This Example describes the isolation of prostate tumor polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library was constructed from prostate tumor poly A<sup>+</sup> RNA using a Superscript Plasmid System for cDNA Synthesis and Plasmid Cloning kit (BRL Life Technologies, Gaithersburg, MD 20897) following the manufacturer's protocol. Specifically, prostate tumor tissues were homogenized with polytron (Kinematica, Switzerland) and total RNA was extracted using Trizol reagent (BRL Life Technologies) as directed by the manufacturer. The poly A<sup>+</sup> RNA was then purified using a Qiagen oligotex spin column mRNA purification kit (Qiagen, Santa Clarita, CA 91355) according to the manufacturer's protocol. First-strand cDNA was synthesized using the NotI/Oligo-dT18 primer. Double-stranded cDNA was synthesized, ligated with EcoRI/BAXI adaptors (Invitrogen, San Diego, CA) and digested with NotI. Following size fractionation with Chroma Spin-1000 columns (Clontech, Palo Alto, CA 94303), the cDNA was ligated into the EcoRI/NotI site of pCDNA3.1 (Invitrogen) and transformed into ElectroMax *E. coli* DH10B cells (BRL Life Technologies) by electroporation.

Using the same procedure, a normal human pancreas cDNA expression library was prepared from a pool of six tissue specimens (Clontech). The cDNA libraries were characterized by determining the number of independent colonies, the percentage of clones that carried insert, the average insert size and by sequence analysis. The prostate tumor library contained  $1.64 \times 10^7$  independent colonies, with 70% of clones having an insert and the average insert size being 1745 base pairs. The normal pancreas cDNA library contained  $3.3 \times 10^6$  independent colonies, with 69% of clones having inserts and the average insert size

being 1120 base pairs. For both libraries, sequence analysis showed that the majority of clones had a full length cDNA sequence and were synthesized from mRNA, with minimal rRNA and mitochondrial DNA contamination.

cDNA library subtraction was performed using the above prostate tumor and normal pancreas cDNA libraries, as described by Hara et al. (*Blood*, 84:189-199, 1994) with some modifications. Specifically, a prostate tumor-specific subtracted cDNA library was generated as follows. Normal pancreas cDNA library (70 µg) was digested with EcoRI, NotI, and SfuI, followed by a filling-in reaction with DNA polymerase Klenow fragment. After phenol-chloroform extraction and ethanol precipitation, the DNA was dissolved in 100 µl of H<sub>2</sub>O, heat-denatured and mixed with 100 µl (100 µg) of Photoprobe biotin (Vector Laboratories, Burlingame, CA). As recommended by the manufacturer, the resulting mixture was irradiated with a 270 W sunlamp on ice for 20 minutes. Additional Photoprobe biotin (50 µl) was added and the biotinylation reaction was repeated. After extraction with butanol five times, the DNA was ethanol-precipitated and dissolved in 23 µl H<sub>2</sub>O to form the driver DNA.

To form the tracer DNA, 10 µg prostate tumor cDNA library was digested with BamHI and XhoI, phenol chloroform extracted and passed through Chroma spin-400 columns (Clontech). Following ethanol precipitation, the tracer DNA was dissolved in 5 µl H<sub>2</sub>O. Tracer DNA was mixed with 15 µl driver DNA and 20 µl of 2 x hybridization buffer (1.5 M NaCl/10 mM EDTA/50 mM HEPES pH 7.5/0.2% sodium dodecyl sulfate), overlaid with mineral oil, and heat-denatured completely. The sample was immediately transferred into a 68 °C water bath and incubated for 20 hours (long hybridization [LH]). The reaction mixture was then subjected to a streptavidin treatment followed by phenol/chloroform extraction. This process was repeated three more times. Subtracted DNA was precipitated, dissolved in 12 µl H<sub>2</sub>O, mixed with 8 µl driver DNA and 20 µl of 2 x hybridization buffer, and subjected to a hybridization at 68 °C for 2 hours (short hybridization [SH]). After removal of biotinylated double-stranded DNA, subtracted cDNA was ligated into BamHI/XhoI site of chloramphenicol resistant pBCSK<sup>+</sup> (Stratagene, La Jolla, CA 92037) and transformed into ElectroMax *E. coli* DH10B cells by electroporation to generate a prostate tumor specific subtracted cDNA library(prostate subtraction 1.

To analyze the subtracted cDNA library, plasmid DNA was prepared from 100 independent clones, randomly picked from the subtracted prostate tumor specific library and grouped based on insert size. Representative cDNA clones were further characterized by DNA sequencing with a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A (Foster City, CA). Six cDNA clones, hereinafter referred to as F1-13, F1-12, F1-16, H1-1, H1-9 and H1-4, were shown to be abundant in the subtracted prostate-specific cDNA library. The determined 3' and 5' cDNA sequences for F1-12 are provided in SEQ ID NO: 2 and 3, respectively, with determined 3' cDNA sequences for F1-13, F1-16, H1-1, H1-9 and H1-4 being provided in SEQ ID No: 1 and 4-7, respectively.

The cDNA sequences for the isolated clones were compared to known sequences in the gene bank using the EMBL and GenBank databases (release 96). Four of the prostate tumor cDNA clones, F1-13, F1-16, H1-1, and H1-4, were determined to encode the following previously identified proteins: prostate specific antigen (PSA), human glandular kallikrein, human tumor expression enhanced gene, and mitochondria cytochrome C oxidase subunit II. H1-9 was found to be identical to a previously identified human autonomously replicating sequence. No significant homologies to the cDNA sequence for F1-12 were found.

Subsequent studies led to the isolation of a full-length cDNA sequence for F1-12. This sequence is provided in SEQ ID NO: 107, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 108.

To clone less abundant prostate tumor specific genes, cDNA library subtraction was performed by subtracting the prostate tumor cDNA library described above with the normal pancreas cDNA library and with the three most abundant genes in the previously subtracted prostate tumor specific cDNA library: human glandular kallikrein, prostate specific antigen (PSA), and mitochondria cytochrome C oxidase subunit II. Specifically, 1  $\mu$ g each of human glandular kallikrein, PSA and mitochondria cytochrome C oxidase subunit II cDNAs in pCDNA3.1 were added to the driver DNA and subtraction was performed as described above to provide a second subtracted cDNA library hereinafter referred to as the "subtracted prostate tumor specific cDNA library with spike".

Twenty-two cDNA clones were isolated from the subtracted prostate tumor specific cDNA library with spike. The determined 3' and 5' cDNA sequences for the clones referred to as J1-17, L1-12, N1-1862, J1-13, J1-19, J1-25, J1-24, K1-58, K1-63, L1-4 and L1-14 are provided in SEQ ID Nos: 8-9, 10-11, 12-13, 14-15, 16-17, 18-19, 20-21, 22-23, 24-25, 26-27 and 28-29, respectively. The determined 3' cDNA sequences for the clones referred to as J1-12, J1-16, J1-21, K1-48, K1-55, L1-2, L1-6, N1-1858, N1-1860, N1-1861, N1-1864 are provided in SEQ ID Nos: 30-40, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to three of the five most abundant DNA species, (J1-17, L1-12 and N1-1862; SEQ ID Nos: 8-9, 10-11 and 12-13, respectively). Of the remaining two most abundant species, one (J1-12; SEQ ID NO:30) was found to be identical to the previously identified human pulmonary surfactant-associated protein, and the other (K1-48; SEQ ID NO:33) was determined to have some homology to *R. norvegicus* mRNA for 2-arylpropionyl-CoA epimerase. Of the 17 less abundant cDNA clones isolated from the subtracted prostate tumor specific cDNA library with spike, four (J1-16, K1-55, L1-6 and N1-1864; SEQ ID Nos:31, 34, 36 and 40, respectively) were found to be identical to previously identified sequences, two (J1-21 and N1-1860; SEQ ID Nos: 32 and 38, respectively) were found to show some homology to non-human sequences, and two (L1-2 and N1-1861; SEQ ID Nos: 35 and 39, respectively) were found to show some homology to known human sequences. No significant homologies were found to the polypeptides J1-13, J1-19, J1-24, J1-25, K1-58, K1-63, L1-4, L1-14 (SEQ ID Nos: 14-15, 16-17, 20-21, 18-19, 22-23, 24-25, 26-27, 28-29, respectively).

Subsequent studies led to the isolation of full length cDNA sequences for J1-17, L1-12 and N1-1862 (SEQ ID NOS: 109-111, respectively). The corresponding predicted amino acid sequences are provided in SEQ ID NOS: 112-114.

In a further experiment, four additional clones were identified by subtracting a prostate tumor cDNA library with normal prostate cDNA prepared from a pool of three normal prostate poly A+ RNA (prostate subtraction 2). The determined cDNA sequences for these clones, hereinafter referred to as U1-3064, U1-3065, V1-3692 and 1A-3905, are provided in SEQ ID NO: 69-72, respectively. Comparison of the determined sequences with those in the gene bank revealed no significant homologies to U1-3065.

A second subtraction with spike (prostate subtraction spike 2) was performed by subtracting a prostate tumor specific cDNA library with spike with normal pancreas cDNA library and further spiked with PSA, J1-17, pulmonary surfactant-associated protein, mitochondrial DNA, cytochrome c oxidase subunit II, N1-1862, autonomously replicating sequence, L1-12 and tumor expression enhanced gene. Four additional clones, hereinafter referred to as V1-3686, R1-2330, 1B-3976 and V1-3679, were isolated. The determined cDNA sequences for these clones are provided in SEQ ID NO:73-76, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to V1-3686 and R1-2330.

Further analysis of the three prostate subtractions described above (prostate subtraction 2, subtracted prostate tumor specific cDNA library with spike, and prostate subtraction spike 2) resulted in the identification of sixteen additional clones, referred to as 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1G-4734, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4810, 1I-4811, 1J-4876, 1K-4884 and 1K-4896. The determined cDNA sequences for these clones are provided in SEQ ID NOS: 77-92, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to 1G-4741, 1G-4734, 1I-4807, 1J-4876 and 1K-4896 (SEQ ID NOS: 79, 81, 87, 90 and 92, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4807, 1J-4876, 1K-4884 and 1K-4896, provided in SEQ ID NOS: 179-188 and 191-193, respectively, and to the determination of additional partial cDNA sequences for 1I-4810 and 1I-4811, provided in SEQ ID NOS: 189 and 190, respectively.

An additional subtraction was performed by subtracting a normal prostate cDNA library with normal pancreas cDNA (prostate subtraction 3). This led to the identification of six additional clones referred to as 1G-4761, 1G-4762, 1H-4766, 1H-4770, 1H-4771 and 1H-4772 (SEQ ID NOS: 93-98). Comparison of these sequences with those in the gene bank revealed no significant homologies to 1G-4761 and 1H-4771 (SEQ ID NOS: 93 and 97, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4761, 1G-4762, 1H-4766 and 1H-4772 provided in SEQ

ID NOS: 194-196 and 199, respectively, and to the determination of additional partial cDNA sequences for 1H-4770 and 1H-4771, provided in SEQ ID NOS: 197 and 198, respectively.

Subtraction of a prostate tumor cDNA library, prepared from a pool of polyA+ RNA from three prostate cancer patients, with a normal pancreas cDNA library (prostate subtraction 4) led to the identification of eight clones, referred to as 1D-4297, 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280 (SEQ ID NOS: 99-107). These sequences were compared to those in the gene bank as described above. No significant homologies were found to 1D-4283 and 1D-4304 (SEQ ID NOS: 103 and 104, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280, provided in SEQ ID NOS: 200-206, respectively.

cDNA clones isolated in prostate subtraction 1 and prostate subtraction 2, described above, were colony PCR amplified and their mRNA expression levels in prostate tumor, normal prostate and in various other normal tissues were determined using microarray technology (Synteni, Palo Alto, CA). Briefly, the PCR amplification products were dotted onto slides in an array format, with each product occupying a unique location in the array. mRNA was extracted from the tissue sample to be tested, reverse transcribed, and fluorescent-labeled cDNA probes were generated. The microarrays were probed with the labeled cDNA probes, the slides scanned and fluorescence intensity was measured. This intensity correlates with the hybridization intensity. Two novel clones (referred to as P509S and P510S) were found to be over-expressed in prostate tumor and normal prostate and expressed at low levels in all other normal tissues tested (liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon). The determined cDNA sequences for P509S and P510S are provided in SEQ ID NO: 223 and 224, respectively. Comparison of these sequences with those in the gene bank as described above, revealed some homology to previously identified ESTs.

## EXAMPLE 2

## DETERMINATION OF TISSUE SPECIFICITY OF PROSTATE TUMOR POLYPEPTIDES

Using gene specific primers, mRNA expression levels for the representative prostate tumor polypeptides F1-16, H1-1, J1-17, L1-12, F1-12 and N1-1862 were examined in a variety of normal and tumor tissues using RT-PCR.

Briefly, total RNA was extracted from a variety of normal and tumor tissues using Trizol reagent as described above. First strand synthesis was carried out using 1-2  $\mu$ g of total RNA with SuperScript II reverse transcriptase (BRL Life Technologies) at 42 °C for one hour. The cDNA was then amplified by PCR with gene-specific primers. To ensure the semi-quantitative nature of the RT-PCR,  $\beta$ -actin was used as an internal control for each of the tissues examined. First, serial dilutions of the first strand cDNAs were prepared and RT-PCR assays were performed using  $\beta$ -actin specific primers. A dilution was then chosen that enabled the linear range amplification of the  $\beta$ -actin template and which was sensitive enough to reflect the differences in the initial copy numbers. Using these conditions, the  $\beta$ -actin levels were determined for each reverse transcription reaction from each tissue. DNA contamination was minimized by DNase treatment and by assuring a negative PCR result when using first strand cDNA that was prepared without adding reverse transcriptase.

mRNA Expression levels were examined in four different types of tumor tissue (prostate tumor from 2 patients, breast tumor from 3 patients, colon tumor, lung tumor), and sixteen different normal tissues, including prostate, colon, kidney, liver, lung, ovary, pancreas, skeletal muscle, skin, stomach, testes, bone marrow and brain. F1-16 was found to be expressed at high levels in prostate tumor tissue, colon tumor and normal prostate, and at lower levels in normal liver, skin and testes, with expression being undetectable in the other tissues examined. H1-1 was found to be expressed at high levels in prostate tumor, lung tumor, breast tumor, normal prostate, normal colon and normal brain, at much lower levels in normal lung, pancreas, skeletal muscle, skin, small intestine, bone marrow, and was not detected in the other tissues tested. J1-17 and L1-12 appear to be specifically over-expressed in prostate, with both genes being expressed at high levels in prostate tumor and normal prostate but at low to undetectable levels in all the other tissues

examined. N1-1862 was found to be over-expressed in 60% of prostate tumors and detectable in normal colon and kidney. The RT-PCR results thus indicate that F1-16, H1-1, J1-17, N1-1862 and L1-12 are either prostate specific or are expressed at significantly elevated levels in prostate.

Further RT-PCR studies showed that F1-12 is over-expressed in 60% of prostate tumors, detectable in normal kidney but not detectable in all other tissues tested. Similarly, R1-2330 was shown to be over-expressed in 40% of prostate tumors, detectable in normal kidney and liver, but not detectable in all other tissues tested. U1-3064 was found to be over-expressed in 60% of prostate tumors, and also expressed in breast and colon tumors, but was not detectable in normal tissues.

RT-PCR characterization of R1-2330, U1-3064 and 1D-4279 showed that these three antigens are over-expressed in prostate and/or prostate tumors.

Northern analysis with four prostate tumors, two normal prostate samples, two BPH prostates, and normal colon, kidney, liver, lung, pancreas, skeletal muscle, brain, stomach, testes, small intestine and bone marrow, showed that L1-12 is over-expressed in prostate tumors and normal prostate, while being undetectable in other normal tissues tested. J1-17 was detected in two prostate tumors and not in the other tissues tested. N1-1862 was found to be over-expressed in three prostate tumors and to be expressed in normal prostate, colon and kidney, but not in other tissues tested. F1-12 was found to be highly expressed in two prostate tumors and to be undetectable in all other tissues tested.

The micro-array technology described above was used to determine the expression levels of representative antigens described herein in prostate tumor, breast tumor and the following normal tissues: prostate, liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon. L1-12 was found to be over-expressed in normal prostate and prostate tumor, with some expression being detected in normal skeletal muscle. Both J1-12 and F1-12 were found to be over-expressed in prostate tumor, with expression being lower or undetectable in all other tissues tested. N1-1862 was found to be expressed at high levels in prostate tumor and normal prostate, and at low levels in normal large intestine and normal colon, with expression being undetectable in all other tissues tested. R1-2330 was found to

be over-expressed in prostate tumor and normal prostate, and to be expressed at lower levels in all other tissues tested. 1D-4279 was found to be over-expressed in prostate tumor and normal prostate, expressed at lower levels in normal spinal cord, and to be undetectable in all other tissues tested.

### Example 3

#### ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES BY PCR-BASED SUBTRACTION

A cDNA subtraction library, containing cDNA from normal prostate subtracted with ten other normal tissue cDNAs (brain, heart, kidney, liver, lung, ovary, placenta, skeletal muscle, spleen and thymus) and then submitted to a first round of PCR amplification, was purchased from Clontech. This library was subjected to a second round of PCR amplification, following the manufacturer's protocol. The resulting cDNA fragments were subcloned into the vector pT7 Blue T-vector (Novagen, Madison, WI) and transformed into XL-1 Blue MRF' *E. coli* (Stratagene). DNA was isolated from independent clones and sequenced using a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A.

Fifty-nine positive clones were sequenced. Comparison of the DNA sequences of these clones with those in the gene bank, as described above, revealed no significant homologies to 25 of these clones, hereinafter referred to as P5, P8, P9, P18, P20, P30, P34, P36, P38, P39, P42, P49, P50, P53, P55, P60, P64, P65, P73, P75, P76, P79, and P84. The determined cDNA sequences for these clones are provided in SEQ ID NO:41-45, 47-52 and 54-65, respectively. P29, P47, P68, P80 and P82 (SEQ ID NO:46, 53 and 66-68, respectively) were found to show some degree of homology to previously identified DNA sequences. To the best of the inventors' knowledge, none of these sequences have been previously shown to be present in prostate.

Further studies using the PCR-based methodology described above resulted in the isolation of more than 180 additional clones, of which 23 clones were found to show no significant

homologies to known sequences. The determined cDNA sequences for these clones are provided in SEQ ID NO: 115-123, 127, 131, 137, 145, 147-151, 153, 156-158 and 160. Twenty-three clones (SEQ ID NO: 124-126, 128-130, 132-136, 138-144, 146, 152, 154, 155 and 159) were found to show some homology to previously identified ESTs. An additional ten clones (SEQ ID NO: 161-170) were found to have some degree of homology to known genes. An additional clone, referred to as P703, was found to have five splice variants. The determined DNA sequence for the variants referred to as DE1, DE13 and DE14 are provided in SEQ ID NOS: 171, 175 and 177, respectively, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 172, 176 and 178, respectively. The DNA sequences for the splice variants referred to as DE2 and DE6 are provided in SEQ ID NOS: 173 and 174, respectively.

mRNA Expression levels for representative clones in tumor tissues (prostate (n=5), breast (n=2), colon and lung) normal tissues (prostate (n=5), colon, kidney, liver, lung (n=2), ovary (n=2), skeletal muscle, skin, stomach, small intestine and brain), and activated and non-activated PBMC was determined by RT-PCT as described above. Expression was examined in one sample of each tissue type unless otherwise indicated.

P9 was found to be highly expressed in normal prostate and prostate tumor compared to all normal tissues tested except for normal colon which showed comparable expression. P20 was found to be highly expressed in normal prostate and prostate tumor, compared to all twelve normal tissues tested. A modest increase in expression of P20 in breast tumor (n=2), colon tumor and lung tumor was seen compared to all normal tissues except lung (1 of 2). Increased expression of P18 was found in normal prostate, prostate tumor and breast tumor compared to other normal tissues except lung and stomach. A modest increase in expression of P5 was observed in normal prostate compared to most other normal tissues. However, some elevated expression was seen in normal lung and PBMC. Elevated expression of P5 was also observed in prostate tumors (2 of 5), breast tumor and one lung tumor sample. For P30, similar expression levels were seen in normal prostate and prostate tumor, compared to six of twelve other normal tissues tested. Increased expression was seen in breast tumors, one lung tumor sample and one colon tumor sample, and also in normal PBMC. P29 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5

of 5) compared to the majority of normal tissues. However, substantial expression of P29 was observed in normal colon and normal lung (2 of 2). P80 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) compared to all other normal tissues tested, with increased expression also being seen in colon tumor.

Further studies using the above methodology resulted in the isolation of twelve additional clones, hereinafter referred to as 10-d8, 10-h10, 11-c8, 7-g6, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3, 8-h11, g-f12 and g-f3. The determined DNA sequences for 10-d8, 10-h10, 11-c8, 8-d4, 8-d9, 8-h11, g-f12 and g-f3 are provided in SEQ ID NO: 207, 208, 209, 216, 217, 220, 221 and 222, respectively. The determined forward and reverse DNA sequences for 7-g6, 8-b5, 8-b6 and 8-g3 are provided in SEQ ID NO: 210 and 211; 212 and 213; 214 and 215; and 218 and 219, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to the sequences of 7-g6 and g-f3. The clones 10-d8, 11-c8 and 8-h11 were found to show some homology to previously isolated ESTs, while 10-h10, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3 and g-f12 were found to show some homology to previously identified genes.

#### EXAMPLE 4

#### SYNTHESIS OF POLYPEPTIDES

Polypeptides may be synthesized on an Applied Biosystems 430A peptide synthesizer using FMOC chemistry with HPTU (O-Benzotriazole-N,N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of conjugation, binding to an immobilized surface, or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of 0%-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to elute the peptides. Following

lyophilization of the pure fractions, the peptides may be characterized using electrospray or other types of mass spectrometry and by amino acid analysis.

From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for the purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention.

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANTS: Xu, Jiangchun  
Dillon, Davin C.

(ii) TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER  
AND METHODS FOR THEIR USE

(iii) NUMBER OF SEQUENCES: 224

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(C) CITY: Seattle  
(D) STATE: WA  
(E) COUNTRY: USA  
(F) ZIP: 98104

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE: 23-FEB-1998  
(C) CLASSIFICATION:

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Maki, David J.  
(B) REGISTRATION NUMBER: 31,392  
(C) REFERENCE/DOCKET NUMBER: 210121.428C3

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(A) TELEPHONE: (206) 622-4900  
(B) TELEFAX: (206) 682-6031

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 814 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTTTTTTTTT TTTTTCACAG TATAACAGCT CTTTATTTCT GTGAGTTCTA CTAGGAAATC

ATCAAATCTG	AGGGTTGTCT	GGAGGACTTC	AATAACACCTC	CCCCCATAGT	GAATCAGCTT	120
CCAGGGGGTC	CAGTCCTCT	CCTTACTTCA	TCCCCATCCC	ATGCCAAAGG	AAGACCCCTCC	180
CTCCTTGGCT	CACAGCCTTC	TCTAGGCTTC	CCAGTGCCTC	CAGGACAGAG	TGGGTTATGT	240
TTTCAGCTCC	ATCCTGCTG	TGAGTGTCTG	GTGCCTTGTG	CCTCCAGCTT	CTGCTCAGTG	300
CTTCATGGAC	AGTGTCCAGC	ACATGTCACT	CTCCACTCTC	TCAGTGTGGA	TCCACTAGTT	360
CTAGAGCGGC	CGCCACCGCG	GTGGAGCTCC	AGCTTTGTT	CCCTTTAGTG	AGGGTTAATT	420
GCGCGCTTGG	CGTAATCATG	GTCATAACTG	TTTCTGTGT	GAAATTGTTA	TCCGCTCACA	480
ATTCCACACA	ACATACGAGC	CGGAAGCATA	AAGTGTAAAG	CCTGGGGTGC	CTAATGAGTG	540
ANCTAACTCA	CATTAATTGC	GTTGCGCTCA	CTGNCCGCTT	TCCAGTCNGG	AAAACGTGCG	600
TGCCAGCTGC	ATTAATGAAT	CGGCCAACGC	NCGGGGAAAA	GCGGTTTGCG	TTTTGGGGC	660
TCTTCCGCTT	CTCGCTCACT	NANTCCTGCG	CTCGGTCTT	CGGCTGCGGG	GAACGGTATC	720
ACTCCTCAAA	GGNGGTATTA	CGGTTATCCN	NAAATCNGGG	GATACCCNGG	AAAAAANTTT	780
AACAAAAGGG	CANCAAAGGG	CNGAAACGTA	AAAA			814

## (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ACAGAAATGT	TGGATGGTGG	AGCACCTTTC	TATACGACTT	ACAGGACAGC	AGATGGGAA	60
TTCATGGCTG	TTGGACCAAT	AGAACCCCCAG	TTCTACGAGC	TGCTGATCAA	AGGACTTGGG	120
CTAAAGTCTG	ATGAACCTCC	CAATCAGATG	AGCATGGATG	ATTGGCCAGA	AATGAAGAAG	180
AAGTTTGCAG	ATGTATTTCG	AAAGAAGACG	AAGGCAGAGT	GGTGTCAAAT	CTTTGACGGC	240
ACAGATGCCT	GTGTGACTCC	GGTTCTGACT	TTTGAGGAGG	TTGTTCATCA	TGATCACAAC	300
AAGGAACGGG	GCTCGTTAT	CACCACTGAG	GAGCAGGAGC	TGAGCCCCCG	CCCTGCACCT	360
CTGCTGTTAA	ACACCCCAGC	CATCCCTTCT	TTCAAAAGGG	ATCCACTAGT	TCTAGAAGCG	420
GCCGCCACCG	CGGTGGAGCT	CCAGCTTTG	TTCCCTTTAG	TGAGGGTTAA	TTGCGCGCTT	480
GGCGTAATCA	TGGTCATAGC	TGTTTCTGT	GTGAAATTGT	TATCCGCTCA	CAATTCCCC	540
AAACATACGAG	CCGGAACATA	AAAGTGTAAAG	CCTGGGGTGC	CTAATGANTG	AGCTAACTCN	600
CATTAATTGC	GTTGCGCTCA	CTGCCCGCTT	TCCAGTCGGG	AAAACGTGCG	TGCCACTGCN	660
TTANTGAATC	NGCCACCCCC	CGGGAAAAGG	CGGTTGCNTT	TTGGGCCTCT	TCCGCTTCC	720
TCGCTCATTG	ATCCTNGCNC	CCGGTCTTCG	GCTGCGGNGA	ACGGTTCACT	CCTCAAAGGC	780
GGTNTNCCGG	TTATCCCCAA	ACNGGGGATA	CCCNGA			816

## (2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 773 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTTTTGAAAG	AAGGGATGGC	TGGGTGTTT	AACAGCAGAG	GTGCAGGGCG	GGGGCTCACG	60
TCCTGCTCCT	CACTGGTGAT	AAACGAGCCC	CGTTCTTGT	TGTGATCATG	ATGAACAACC	120

TCCTCAAAAG	TCAGAACCGG	AGTCACACAG	GCATCTGTGC	CGTCAAAGAT	TTGACACCAC	180
TCTGCCCTCG	TCTTCTTGC	AAATACATCT	GCAAACATTCT	TCTTCATTTC	TGGCCAATCA	240
TCCATGCTCA	TCTGATTGGG	AAGTTCATCA	GACTTTAGTC	CANNTCCCTT	GATCAGCAGC	300
TCGTAGAACT	GGGGTTCTAT	TGCTCCAACA	GCCATGAATT	CCCCATCTGC	TGTCCGTAA	360
GTCGTATAGA	AAGGTGCTCC	ACCATCCAAC	ATGTTCTGTG	CTCGAGGGGG	GGCCCCGGTAC	420
CCAATTGCC	CTATANTGAG	TGTTATTACG	CGCGCTCACT	GGCCGTCGTT	TTACAACGTC	480
GTGACTGGGA	AAACCCCTGGG	CGTTACCAAC	TTAACCGCCT	TGCAGCACAT	CCCCCTTCG	540
CCAGCTGGGC	GTAATANCGA	AAAGGCCCGC	ACCGATCGCC	CTTCCAACAG	TTGCGCACCT	600
GAATGGGNAA	ATGGGACCCC	CCTGTTACCG	CGCATTAAC	CCCCGCNGGG	TTTNGTTGTT	660
ACCCCCACNT	NNACCGCTTA	CACTTTGCCA	GCGCCTTANC	GCCCCTCCTCC	TTTCNCCTTT	720
CTTCCCTTCC	TTTCNCNCCN	CTTCCCCCG	GGGTTCCCC	CNTCAAACCC	CNA	773

## (2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 828 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCTCCCTGAGT	CCTACTGACC	TGTGCTTTCT	GGTGTGGAGT	CCAGGGCTGC	TAGGAAAAGG	60
AATGGGCAGA	CACAGGTGTA	TGCCAATGTT	TCTGAAATGG	GTATAATTTC	GTCCTCTCCT	120
TCGGAACACT	GGCTGTCTCT	GAAGACTTCT	CGCTCAGTTT	CAGTGAGGAC	ACACACAAAG	180
ACGTGGGTGA	CCATGTTGTT	TGTGGGGTGC	AGAGATGGG	GGGGTGGGGC	CCACCCCTGGA	240
AGAGTGGACA	GTGACACAAG	GTGGACACTC	TCTACAGATC	ACTGAGGATA	AGCTGGAGCC	300
ACAATGCATG	AGGCACACAC	ACAGCAAGGA	TGACNCTGTA	AACATAGCCC	ACGCTGTCCT	360
GNNGGCACTG	GGAAGCCTAN	ATNAGGCCGT	GAGCANAAG	AAGGGGAGGA	TCCACTAGTT	420
CTANAGCGGC	CGCCACCGCG	GTGGANCTCC	ANCTTTGTT	CCCTTTAGTG	AGGGTTAATT	480
GCGCGCTTGG	CNTAACATG	GTCATANCTN	TTTCCTGTGT	GAAATTGTTA	TCCGCTCACA	540
ATTCCACACA	ACATACGANC	CGGAAACATA	AANTGTAAAC	CTGGGGTGCC	TAATGANTGA	600
CTAACTCACA	TTAACATTGCGT	TGCGCTCACT	GCCCGCTTTC	CAATCNGGAA	ACCTGCTTIG	660
CNCNTTGCA	TNATGAATCN	GCCAACCCCC	GGGGAAAAGG	GTTTGCCTTT	TGGGCCTCT	720
TCCGCTTCCCT	CNCTCANTTA	NTCCCTNCNC	TCGGTCATTG	CGGCTGCNGC	AAACCGGTTCA	780
ACCNCCCTCCA	AAGGGGTAT	TCCGGTTTCC	CCNAATCCGG	GGANANCC		828

## (2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 834 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TTTTTTTTTT	TTTTTACTGA	TAGATGGAAT	TTATTAAGCT	TTTCACATGT	GATAGCACAT	60
AGTTTTAATT	GCATCCAAAG	TACTAACAA	AACTCTAGCA	ATCAAGAATG	GCAGCATGTT	120
ATTTTATAAC	AATCAACACC	TGTGGCTTTT	AAAATTGTT	TTTCATAAGA	TAATTTATAC	180
TGAAGTAAAT	CTAGCCATGC	TTTTAAAAAA	TGCTTTAGGT	CACTCCAAGC	TTGGCAGTTA	240

ACATTTGGCA TAAACAATAA TAAAACAATC ACAATTAAAT AAATAACAAA TACAACATTG	300
TAGGCCATAA TCATATACAG TATAAGGAAA AGGTGGTAGT GTTGAGTAAG CAGTTATTAG	360
AATAGAATAC CTTGGCCTCT ATGCAAATAT GTCTAGACAC TTTGATTAC TCAGCCCTGA	420
CATTCAAGTT TCAAAGTAGG AGACAGGTT TACAGTATCA TTTTACAGTT TCCAACACAT	480
TGAAAACAAG TAGAAAATGA TGAGTTGATT TTTATTAAATG CATTACATCC TCAAGAGTTA	540
TCACCAACCC CTCAGTTATA AAAAATTTTC AAGTTATATT AGTCATATAA CTTGGTGTGC	600
TTATTTAAA TTAGTGCTAA ATGGATTAAG TGAAGACAAC AATGGTCCCC TAATGTGATT	660
GATATTGGTC ATTTTACCA GCTTCTAAAT CTNAACTTTC AGGCTTTGGA ACTGGAACAT	720
TGNATNACAG TGTCCANAG TTNCAACCTA CTGGAACATT ACAGTGTGCT TGATTCAAAA	780
TGTTATTTTG TAAAAAATTA AATTTAACC TGGTGGAAAAA ATAATTTGAA ATNA	834

## (2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 818 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTTTTTTTTT TTTTTTTTTT AAGACCCTCA TCAATAGATG GAGACATACA GAAATAGTCA	60
AACCACATCT ACAAAATGCC AGTATCAGGC GGCAGCTTCG AACCCAAAGT GATGTTGGA	120
TGAAAGTGA AATATTAGTT GCGGGATGAA GCAGATAGTG AGGAAAGTTG AGCCAATAAT	180
GACGTGAAGT CCGTGGAAAGC CTGTGGCTAC AAAAATGTT GAGCCGTAGA TGCGTCGGA	240
AATGGTGAAG GGAGACTCGA AGTACTCTGA GGCTTGAGG AGGGTAAAAT AGAGACCCAG	300
TAAAATTGTA ATAAGCAGTG CTTGAATTAT TTGGTTTCGG TTGTTTCTA TTAGACTATG	360
GTGAGCTCAG GTGATTGATA CTCCTGATGC GAGTAATACG GATGTGTTA GGAGTGGAC	420
TTCTAGGGGA TTTAGGGGG TGATGCCTGT TGGGGCCAG TGCCCTCCTA GTTGGGGGT	480
AGGGGCTAGG CTGGAGTGGT AAAAGGCTCA GAAAAATCCT GCGAAGAAAA AAACCTCTGA	540
GGTAATAAT AGGATTATCC CGTATCGAAG GCCTTTTGG ACAGGGTGGTG TGTGGTGGCC	600
TTGGTATGTG CTTTCTCGTG TTACATCGCG CCATCATTGG TATATGGTTA GTGTGTTGGG	660
TTANTANGGC CTANTATGAA GAACTTTGG ANTGGAAATTA AATCAATNGC TTGGCCGGAA	720
GTCATTANGA NGGCTNAAA GGCCTGTTA NGGGCTGGG CTNGGTTTTA CCCNACCCAT	780
GGAATNCNCC CCCCCGACNA NTGNATCCCT ATTCTTAA	818

## (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 817 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TTTTTTTTTT TTTTTTTTTT TGGCTCTAGA GGGGGTAGAG GGGGTGCTAT AGGGTAAATA	60
CGGGCCCTAT TTCAAAGATT TTAGGGGAA TTAATTCTAG GACGATGGGT ATGAAACTGT	120
GGTTTGCTCC ACAGATTCA GAGCATTGAC CGTAGTATAC CCCCGGTCGT GTAGCGGTGA	180
AAAGGGTTTG GTTTAGACGT CCGGGAATTG CATCTGTTT TAAGCCTAAT GTGGGGACAG	240
CTCATGAGTG CAAGACGCT TGTGATGTAA TTATTATACN AATGGGGCCT TCAATCGGGA	300

GTACTACTCG ATTGTCAACG TCAAGGAGTC GCAGGTCGCC TGGTTCTAGG AATAATGGGG	360
GAAGTATGTA GGAATTGAAG ATTAATCCGC CGTAGTCGGT GTTCTCCTAG GTTCAATACC	420
ATTGGTGGCC AATTGATTTG ATGGTAAGGG GAGGGATCGT TGAACTCGTC TGTTATGTAA	480
AGGATNCCTT NGGGATGGGA AGGCNATNAA GGACTANGGA TNAATGGCGG GCANGATATT	540
TCAAACNGTC TCTANTTCCT GAAACGTCTG AAATGTTAAT AANAATTAAAN TTTNGTTATT	600
GAATNTTNG GAAAAGGGCT TACAGGACTA GAAACCAAAT ANGAAAANTA ATNNNTAANGG	660
CNTTATCNTN AAAGGTNATA ACCNCTCCTA TNATCCCACC CAATNGNATT CCCCCACNCNN	720
ACNATTGGAT NCCCCANTTC CANAAANGGC CNCCCCCGG TGNANNCCNC CTTTTGTTCC	780
CTTNANTGAN GGTTATTNC CCCTNGCNTT ATCANCC	817

## (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CATTTCCGGG TTTACTTTCT AAGGAAAGCC GAGCGGAAGC TGCTAACGTG GGAATCGGTG	60
CATAAGGAGA ACTTTCTGCT GGCACCGCCT AGGGACAAGC GGGAGAGCGA CTCCGAGCGT	120
CTGAAGCGCA CGTCCCAGAA GGTGGACTTG GCACGTAAAC AGCTGGGACA CATCCGCGAG	180
TACGAACAGC GCCTGAAAGT GCTGGAGCGG GAGGTCCAGC AGTGTAGCCG CGTCCTGGGG	240
TGGGTGGCCG ANGCCTGANC CGCTCTGCCT TGCTGCCCCC ANGTGGCCG CCACCCCCCTG	300
ACCTGCCTGG GTCCAAACAC TGAGCCCTGC TGGCGGACTT CAAGGANAAC CCCCACANGG	360
GGATTTTGCT CCTANANTAA GGCTCATCTG GGCCTCGGCC CCCCCACCTG GTTGGCCTTG	420
TCTTTGANGT GAGCCCCATG TCCATCTGGG CCACTGTCNG GACCACCTTT NGGGAGTGTT	480
CTCCTTACAA CCACANNATG CCCGGCTCCT CCCGGAAACC ANTCCCACNC TGNGAAGGAT	540
CAAGNCCTGN ATCCACTNNT NCTANAACCG GCCNCCNCCG CNGTGGAACCC CNCCCTNTGT	600
TCCTTTCTN TNAGGGTTAA TNNCGCCTTG GCCTTNCCAN NGTCCTNCNC NTTTTCCNNT	660
GTTNAAATTG TTANGCNCCC NCCNNTCCCN CNNCNCCNAN CCCGACCCNN ANNTTNANN	720
NCCTGGGGT NCCNNCNGAT TGACCCNNCC NCCCTNTANT TGCNTTNGGG NNCNNNTGCC	780
CTTTCCCTCT NGGGANNCG	799

## (2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ACGCCTTGAT CCTCCCAGGC TGGGACTGGT TCTGGGAGGA GCCGGGCATG CTGTGGTTTG	60
TAANGATGAC ACTCCCAAAG GTGGTCCTGA CAGTGGCCCA GATGGACATG GGGCTCACCT	120
CAAGGACAAG GCCACCAGGT GCGGGGGCCG AAGCCCACAT GATCCTTACT CTATGAGCAA	180
AATCCCTGT GGGGGCTTCT CCTTGAAGTC CGCCANCAGG GCTCAGTCTT TGGACCCANG	240
CAGGTCTAGG GGTTGTNGNC CAACTGGGGG CCNCAACGCA AAANGGCNCA GGGCCTCNGN	300
CACCCATCCC ANGACCGGGC TACACTNCTG GACCTCCNC TCCACCACTT TCATGCGCTG	360

TTCNTACCCG CGNATNTGTC CCANCTGTT CNGTGCCNAC TCCANTTCT NGGACGTGCG	420
CTACATACGC CCGGANTCNC NCTCCCGTT TGTCCTATC CACGTNCCAN CAACAAATT	480
CNCCNTANTG CACCNATTCC CACNTTNNC AGNTTCCNC NNCNGCTTC CTTNTAAAAG	540
GGTTGANCCC CGGAAAATNC CCCAAAGGGG GGGGGCCNNG TACCCAACN CCCCCTNATA	600
GCTGAANTCC CCATNACNN GNCTCNATGG ANCCNTCCNT TTTAANNACN TTCTNAACTT	660
GGGAANANCC CTCGNCNTN CCCCCNTAA TCCCNCCTTG CNANGNNCNT CCCCCNNTCC	720
NCCCNNTNG GCNTTNANN CNAAAAAGGC CCNNNANCAA TCTCCTNNCN CCTCANTTCG	780
CCANCCCTCG AAATCGGCCN C	801

## (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 789 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CAGTCTATNT GGCCAGTGTG GCAGCTTCC CTGTGGCTGC CGGTGCCACA TGCCTGTCCC	60
ACAGTGTGGC CGTGGTACA GCTTCAGCCG CCCTCACCGG GTTCACCTTC TCAGCCCTGC	120
AGATCTGCC CTACACACTG GCCTCCCTCT ACCACCGGGA GAAGCAGGTG TTCCCTGCCA	180
AATACCGAGG GGACACTGGA GGTGCTAGCA GTGAGGACAG CCTGATGACC AGCTTCTGC	240
CAGGCCCTAA GCCTGGAGCT CCCTTCCCTA ATGGACACGT GGGTGCCTGA GGCAGTGGCC	300
TGCTCCACC TCCACCCGCG CTCTGCAGGG CCTCTGCCTG TGATGTCTCC GTACGTGTGG	360
TGGTGGGTGA GCCCACCGAN GCCAGGGTGG TTCCGGGCCG GGGCATCTGC CTGGACCTCG	420
CCATCCTGGA TAGTGCCTCC TGCTGTCCA NGTGGCCCA TCCCTGTTA TGGGCTCCAT	480
TGTCCAGCTC AGCCAGCTG TCACTGCCTA TATGGTGTCT GCGCAGGCC TGGGTCTGGT	540
CCCATTTACT TTGCTACACA GGTANTATT GACAAGAACG ANTTGGCAA ATACTCAGCG	600
TTAAAAAAATT CCAGCACAT TGGGGGTGGA AGGCCTGCCT CACTGGGTCC AACTCCCCGC	660
TCTCTTTAAC CCCATGGGGC TGCCGGCTTG GCGCCAAATT TCTGTTGCTG CCAAANTNAT	720
GTGGCTCTCT GCTGCCACCT GTTGCTGGCT GAAGTGCNTA CNGCNCANCT NGGGGGGTNG	780
GGNGTTCCC	789

## (2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 772 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCCACCCCTAC CCAAATATTA GACACCAACA CAGAAAAGCT AGCAATGGAT TCCCTTCTAC	60
TTTGTAAAT AAATAAGTTA AATATTTAAA TGCTGTGTC TCTGTGATGG CAACAGAAGG	120
ACCAACAGGC CACATCCTGA TAAAAGGTA GAGGGGGGTG GATCAGCAAA AAGACAGTGC	180
TGTGGGCTGA GGGGACCTGG TTCTTGTGTG TTGCCCCCTCA GGACTCTTCC CCTACAAATA	240
ACTTTCATAT GTTCAAATCC CATGGAGGAG TGTTTCATCC TAGAAACTCC CATGCAAGAG	300
CTACATTAAA CGAAGCTGCA GGTAAAGGGG CTTANAGATG GGAAACCAGG TGACTGAGTT	360
TATTCAGCTC CCAAAAACCC TTCTCTAGGT GTGTCTAAC TAGGAGGCTA GCTGTTAAC	420

CTGAGCCTGG	GTAATCCACC	TGCAGAGTCC	CCGCATTCCA	GTGCATGGAA	CCCTTCTGGC	480
CTCCCTGTAT	AAGTCCAGAC	TGAAACCCCC	TTGGAAGGNC	TCCAGTCAGG	CAGCCCTANA	540
AACTGGGAA	AAAAGAAAAG	GACGCCCAN	CCCCCAGCTG	TGCACTACG	CACCTCAACA	600
GCACAGGGTG	GCAGCAAAAA	AACCACTTA	CTTTGGCACA	AACAAAAACT	NGGGGGGGCA	660
ACCCCGGCAC	CCCNANGGG	GTAAACAGGA	ANCNGGGNAA	CNTGGAACCC	AATTNAGGCA	720
GGCCCNCCAC	CCCNAATNTT	GCTGGAAAT	TTTCCTCCC	CTAAATTNTT	TC	772

## (2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 751 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCCCCAATTC	CAGCTGCCAC	ACCACCCACG	GTGACTGCAT	TAGTTCGGAT	GTCATACAAA	60
AGCTGATTGA	AGCAACCCCTC	TACTTTTGG	TCGTGAGCCT	TTTGCTTGGT	GCAGGTTTCA	120
TTGGCTGTGT	TGGTACGTT	GTCATTGCAA	CAGAATGGGG	GAAAGGCACT	GTTCTCTTG	180
AAGTANGGTG	AGTCCTCAAA	ATCCGTATAG	TTGGTGAAGC	CACAGCACTT	GAGCCCTTTC	240
ATGGTGGTGT	TCCACACTTG	AGTGAAGTCT	TCCTGGGAAC	CATAATCTTT	CTTGATGGCA	300
GGCACTACCA	GCAACGTCAG	GGAAAGTGCTC	AGCCATTGTG	GTGTACACCA	AGGCAGGACAC	360
AGCAGCTGCG	ACCTCAGCAA	TGAAGATGAN	GAGGANGATG	AAGAAGAACG	TCNCGAGGGC	420
ACACTTGCTC	TCAGTCTTAN	CACCATANCA	GCCCNTGAAA	ACCAANANCA	AAGACCACNA	480
CNCCGGCTGC	GATGAAGAAA	TNACCCCNCG	TTGACAAACT	TGCATGGCAC	TGGGANCCAC	540
AGTGGCCCN	AAAATCTTCA	AAAAGGATGC	CCCATCNATT	GACCCCCCAA	ATGCCCACTG	600
CCAACAGGGG	CTGCCCCACN	CNCNNAAACGA	TGANCCNATT	GNACAAGATC	TNCNTGGTCT	660
TNATNAACNT	GAACCTGCN	TNGTGGCTCC	TGTTCAAGNC	CNNGGCCTGA	CTTCTNAANN	720
AANGAACTCN	GAAGNCCCCA	CNNGGANANN	CG			751

## (2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 729 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAGCCAGGCG	TCCCTCTGCC	TGCCCACTCA	GTGGCAACAC	CCGGGAGCTG	TTTTGTCCCTT	60
TGTGGANCT	CAGCAGTNCC	CTCTTCAGA	ACTCANTGCC	AAGANCCCTG	AACAGGAGCC	120
ACCATGCAGT	GCTTCAGCTT	CATTAAGACC	ATGATGATCC	TCTTCAATT	GCTCATCTTT	180
CTGTGTGGTG	CAGCCCTGTT	GGCAGTGGGC	ATCTGGGTGT	CAATCGATGG	GGCATCCTTT	240
CTGAAGATCT	TCGGGCCACT	GTCGTCCAGT	GCCATGCAGT	TTGTCACAGT	GGGCTACTTC	300
CTCATCGCAG	CCGGCGTTGT	GGTCTTAGCT	CTAGGTTCC	TGGGCTGCTA	TGGTGCTAAG	360
ACTGAGAGCA	AGTGTGCCCT	CGTGACGTTC	TTCTTCATCC	TCCTCCTCAT	CTTCATTGCT	420
GAGGTTGCAA	TGCTGTGGTC	GCCTTGGTGT	ACACCACAA	GGCTGAGCAC	TTCCTGACGT	480
TGCTGGTAAT	GCCTGCCATC	AANAAAAGAT	TATGGGTTCC	CAGGAANACT	TCACTCAAGT	540
GTTGGAACAC	CACCATGAAA	GGGCTCAAGT	GCTGTGGCTT	CNNCCAACTA	TACGGATTTT	600

GAAGANTCAC CTACTCAAA GAAAANAGTG CCTTTCCCCC ATTTCTGTTG CAATTGACAA	660
ACGTCCCCAA CACAGCCAAT TGAAAACCTG CACCCAACCC AAANGGGTCC CCAACCANAA	720
ATTNAAGGG	729

## (2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGCTCTTCCT CAAAGTTGTT CTTGTTGCCA TAACAACAC CATAAGTAAA GCGGGCGCAG	60
TGTTCGCTGA AGGGGTTGTA GTACCAGCGC GGGATGCTCT CCTTGAGAG TCCTGTGCT	120
GGCAGGTCCA CGCAGTGCCTC TTTGTCACTG GGGAAATGGA TGCAGCTGGAG CTCGTCAAAG	180
CCACTCGTGT ATTTTCACA GGAGCCTCG TCCGACCGT CGGGGCAGTT GGGGGTGTCT	240
TCACACTCCA GGAAACTGTC NATGCAGCAG CCATTGCTGC AGCGGAACGT GGTGGGCTGA	300
CANGTGCCAG AGCACACTGG ATGGCGCTT TCCATGNAN GGGCCCTGNG GGAAAGTCCC	360
TGANCCCCAN ANCTGCCTCT CAAANGCCCC ACCTTGACACA CCCCAGCAGG CTAGAATGGA	420
ATCTTCTTCC CGAAAGGTAG TTNTTCTTGT TGCCCAANCC ANCCCCNTAA ACAAACTCTT	480
GCANATCTGC TCCGNGGGG TCNTANTACC ANCGTGGAA AAGAACCCCA GGCNGCGAAC	540
CAANCTTGTG TGGATNCGAA GCNATAATCT NCTNTCTGC TTGGTGGACA GCACCANTNA	600
CTGTNNANCT TTAGNCCNTG GTCCCTCNGG GTTGNNTTG AACCTAATCN CCNNNTCAACT	660
GGGACAAGGT AANTNGCCNT CTTTNAATT CCCNANCNTN CCCCCTGGTT TGGGGTTTTN	720
CNCNCTCCTA CCCCAGAAAN NCCGTGTTCC CCCCCAACTA GGGGCCNAAA CCNNNTNTTC	780
CACAACCCTN CCCCACCCAC GGTTCTNGNT GGTTNG	816

## (2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 783 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCAAGGCCTG GGCAGGCATA NACTTGAAGG TACAACCCCA GGAACCCCTG GTGCTGAAGG	60
ATGTGGAAAA CACAGATTGG CGCCTACTGC GGGGTGACAC GGATGTCAGG GTAGAGAGGA	120
AAGACCCAAA CCAGGTGGAA CTGTGGGGAC TCAAGGAANG CACCTACCTG TTCCAGCTGA	180
CAGTGAATG CTCAGACCCAC CCAGAGGACA CGGCCAACGT CACAGTCACT GTGCTGTCCA	240
CCAAGCAGAC AGAAGACTAC TGCTCGCAT CCAACAAAGT GGGTCGCTGC CGGGGCTCTT	300
TCCCACGCTG GTACTATGAC CCCACGGAGC AGATCTGCAA GAGTTTCGTT TATGGAGGCT	360
GCTTGGGCAA CAAGAACAAAC TACCTTCGGG AAGAAGAGTG CATTCTANCC TGTCNGGGTG	420
TGCAAGGTGG GCCTTGANA NGCANCTCTG GGGCTCANGC GACTTTCCCC CAGGGCCCT	480
CCATGGAAAG GCGCCATCCA NTGTTCTCTG GCACCTGTCA GCCCACCCAG TTCCGCTGCA	540
NCAATGGCTG CTGCATCNAC ANTTTCCTNG AATTGTGACA ACACCCCCCA NTGCCCCAA	600
CCCTCCCAAC AAAGCTTCCC TGTTNAAAA TACNCCANTT GGCTTTNAC AAACNCCCG	660
CNCCTCCNTT TTCCCCNNTN AACAAAGGGC NCTNGCNTT GAACTGCCN AACCCNGAA	720

TCTNCCNNGG AAAAANTNCC CCCCTGGTT CCTNNAAANCC CCTCCNCNAA ANCTNCCCC	780
CCC	783

## (2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCCCCAATTC CAGCTGCCAC ACCACCCACG GTGACTGCAT TAGTCGGAT GTCATACAAA	60
AGCTGATTGA AGCAACCTC TACTTTTGGG TCGTGAGCCT TTGCTTGGT GCAGGTTTCA	120
TTGGCTGTG TGTTGACGTT GTCATTGCAA CAGAATGGGG GAAAGGCACG TTCTCTTTG	180
AAGTAGGGTG AGTCCTCAAA ATCCGTATAG TTGGTGAAGC CACAGCACTT GAGCCCTTC	240
ATGGTGGTGT TCCACACTTG AGTGAAGTCT TCCTGGGAAC CATAATCTTT CTTGATGGCA	300
GGCACTACCA GCAACGTCAG GAAGTGTCA GCCATTGTGG TGTACACCAA GGCAGACACA	360
GCAGCTGCAA CCTCAGCAAT GAAGATGAGG AGGAGGATGA AGAAGAACGT CNCGAGGGCA	420
CACTTGCTCT CCGTCTTAGC ACCATAGCAG CCCANGAAAC CAAGAGCAAA GACCACAACG	480
CCNGCTGCGA ATGAAAGAAA NTACCCACGT TGACAAACTG CATGGCCACT GGACGACAGT	540
TGGCCCGAAN ATCTTCAGAA AAGGGATGCC CCATCGATTG AACACCCANA TGCCCACCTGC	600
CNACAGGGCT GCNCCNCNCN GAAAGAATGAA GCCATTGAAAG AAGGATCNC NTGGTCTTAA	660
TGAACTGAAA CCNTGCATGG TGGCCCTGT TCAGGGCTCT TGGCAGTGA TTCTGANAAA	720
AAGGAACNGC NTNAGCCCC CCAAANGANA AAACACCCCC GGGTGTGCA CTGAATTGGC	780
GGCCAAGGAN CCCTGCCCN G	801

## (2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 740 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTGAGAGCCA GGCGTCCCTC TGCCTGCCCA CTCAGTGGCA ACACCCGGGA GCTGTTTGT	60
CCTTTGTGGA GCCTCAGCAG TTCCCTCTTT CAGAACTCAC TGCCAAGAGC CCTGAACAGG	120
AGCCACCATG CAGTGCCTCA GCTTCATTAA GACCATGATG ATCCTCTTCA ATTTGCTCAT	180
CTTTCTGTGT GGTGCAGCCC TGGTGGCAGT GGGCATCTGG GTGTCAATCG ATGGGGCATC	240
CTTTCTGAAG ATCTTCGGGC CACTGTCGTC CAGTGCATG CAGTTGTCA ACGTGGCTA	300
CTTCCTCATC GCAGCCGGCG TTGTGGCTTT TGCTCTTGGT TTCCCTGGCT GCTATGGTC	360
TAAGACGGAG AGCAAGTGTG CCCTCGTGAC GTTCTCTTC ATCCCTCCTCC TCATCTTCAT	420
TGCTGAAGTT GCAGCTGCTG TGGTCGCCCTT GGTGTACACC ACAATGGCTG AACCATCCCT	480
GACGTTGCTG GTANTGCCTG CCATCAANAA AGATTATGGG TTCCCAAGGAA AAATTCAC	540
AANTNTGGAA CACCNCCATG AAAAGGGCTC CAATTCTGN TGGCTTCCCC AACTATACCG	600
GAATTTGAA AGANTCNCCTT TACTTCCAAA AAAAAANANT TGCCTTNTCC CCCNTCTGT	660
TGCAATGAAA ACNTCCAAN ACNGCCAATN AAAACCTGCC CNNCAAAAA GGNTCNAAA	720
CAAAAAAANT NNAAGGGTTN	740

## (2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCGCTGGTTG	CGCTGGTCCA	GNGNAGCCAC	GAAGCACGTC	AGCATAACACA	GCCTCAATCA	60
CAAGGTCTTC	CAGCTGCCGC	ACATTACGCA	GGGCAAGAGC	CTCCAGCAAC	ACTGCATATG	120
GGATAACACTT	TACTTTAGCA	GCCAGGGTGA	CAACTGAGAG	GTGTCGAAGC	TTATTCTTCT	180
GAGCCTCTGT	TAGTGGAGGA	AGATTCCGGG	CTTCAGCTAA	GTAGTCAGCG	TATGTCCCAT	240
AAGCAAACAC	TGTGAGCAGC	CGGAAGGTAG	AGGCAAAGTC	ACTCTCAGCC	AGCTCTCTAA	300
CATTGGGCAT	GTCCAGCAGT	TCTCCAAACAA	CGTAGACACC	AGNGGCCTCC	AGCACCTGAT	360
GGATGAGTGT	GGCCAGCGCT	GCCCCCTTGG	CCGACTTGGC	TAGGAGCAGA	AATTGCTCCT	420
GGTTCTGCC	TGTCACCTTC	ACTTCCGCAC	TCATCACTGC	ACTGAGTGTG	GGGGACTTGG	480
GCTCAGGATG	TCCAGAGACG	TGGTTCCGCC	CCCTCNCCTTA	ATGACACCGN	CCANNCAACC	540
GTCGGCTCCC	GCCGANTGNG	TTCGTCGTNC	CTGGGTCAAG	GTCTGCTGGC	CNCTACTTGC	600
AANCTTCGTC	NGGCCCATGG	AATTCAACNC	ACCGGAACTN	GTANGATCCA	CTNNNTCTAT	660
AACCGGNCGC	CACCGCENN	GGAACTCCAC	TCTTNTTNCC	TTTACTTGAG	GGTTAAGGTC	720
ACCCCTNNCG	TTACCTTGGT	CCAAACCN	CCNTGTGTG	ANATNGTNA	TCNGGNCCNA	780
TNCCANCCNC	ATANGAAGCC	NG				802

## (2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CNAAGCTTCC	AGGTNACGGG	CCGCNAANCC	TGACCCNAGG	TANCANAANG	CAGNCNGCGG	60
GAGCCCACCG	TCACGNGGNG	GNGTCTTTAT	NGGAGGGGGC	GGAGCCACAT	CNCTGGACNT	120
CNTGACCCCA	ACTCCCCNCC	NCNCANTGCA	GTGATGAGTG	CAGAACTGAA	GGTNACGTGG	180
CAGGAACCAA	GANCAAANNC	TGCTCCNNTC	CAAGTCGGCN	NAGGGGGCGG	GGCTGGCCAC	240
GCNCATCCNT	CNAGTGTGN	AAAGCCCCNN	CCTGTCTACT	TGTTTGGAGA	ACNGCENNNGA	300
CATGCCCAGN	GTTANATAAC	NGGNGAGAG	TNANTTTGCC	TCTCCCTTCC	GGCTGCGCAN	360
CGNGTNTGCT	TAGNGGACAT	AACTGACTA	CTTAACTGAA	CCCNNGAATC	TNCCNCCCT	420
CCACTAAGCT	CAGAACAAAA	AACTTCGACA	CCACTCANTT	GTCACCTGNC	TGCTCAAGTA	480
AAGTGTACCC	CATNCCCAAT	GTNTGCTNGA	NGCTCTGNCC	TGCNTTANGT	TCGGTCCTGG	540
GAAGACCTAT	CAATTNAAGC	TATGTTCTG	ACTGCCTCTT	GCTCCCTGNA	ACAANCNACC	600
CNNCNNTCCA	AGGGGGGGNC	GGCCCCAAT	CCCCCNAACC	NTNAATTNAN	TTTANCCCN	660
CCCCCNGGCC	CGGCCTTTA	CNANCNTCNN	NNACNGGGNA	AAACCNNNGC	TTTNCCCAAC	720
NNAATCCNCC	T					731

## (2) INFORMATION FOR SEQ ID NO:20:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TTTTTTTTTT	TTTTTTTTTT	TAAAAACCCC	CTCCATTNAA	TGNAACCTTC	CGAAATTGTC	60
CAACCCCCTC	NTCCAAATNN	CNTTTCGG	GNGGGGTTC	CAAACCCAAN	TTANNTTTGG	120
ANNTTAAATT	AAATMTTNNT	TGGNGGNNA	ANCCNAATGT	NANGAAAGTT	NAACCCANTA	180
TNANCTTNA	TNCCTGGAAA	CCNGTNGNTT	CAAAAATNT	TTAACCCCTTA	ANTCCCTCCG	240
AAATNGTTNA	NGGAAAACCC	AANTTCTCNT	AAGGTTGTTT	GAAGGNTNAA	TNAAAANCCC	300
NNCCAATTGT	TTTNGCCAC	GCCTGAATTA	ATTGGNTTCC	GNTGTTTCC	NTTAAAANAA	360
GGNNANCCCC	GGTTANTNAA	TCCCCCCNNC	CCCAATTATA	CCGANNTTTT	TTNGAATTGG	420
GANCCCNCGG	GAATTAACGG	GGNNNNNTCCC	TNTTGGGGGG	CNGGNNCNNC	CCCCNTCGGG	480
GGTTNGGGNC	AGGNCCNAAT	TGTTTAAGGG	TCCGAAAAAT	CCCTCCNAGA	AAAAAAANCTC	540
CCAGGNTGAG	NNTNGGGTTT	NCCCCCCCCC	CANGGGCCCT	CTCGNANAGT	TGGGGTTTGG	600
GGGGCCTGGG	ATTTTNTTTTC	CCCTNTTNCC	TCCCCCCCCC	CCNGGGANAG	AGGTTNGNGT	660
TTTGNTCNNC	GGCCCCNCCN	AAGANTTTN	CCGANTTNAN	TTAAATCCNT	GCCTNGGCAG	720
AGTCCNTTGN	AGGGNTAAAN	GGCCCCCTNN	CGGG			754

## (2) INFORMATION FOR SEQ ID NO:21:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 755 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATCANCCCAT	GACCCNAAC	NNGGGACCNC	TCANCCGNC	NNNCNACCNC	CGGCCNATCA	60
NNGTNAGNNC	ACTNCNNTN	NATCACNCCC	CNCCNACTAC	GCCCNCNANC	CNACGNCTA	120
NNCANATNCC	ACTGAGNGCG	CGANGTNGAN	NGAGAAANCT	NATACCANAG	NCACCANACN	180
CCAGCTGTCC	NANAANGCCT	NNNATACNGG	NNNATCCAAT	NTGNANCCTC	CNAAGTATTN	240
NNCNCNANAT	GATTTCCCTN	ANCCGATTAC	CCNTCCCCC	TANCCCCTCC	CCCCAACNA	300
CGAAGGCNCT	GGNCCNAAGG	NNGCGNCNC	CCGCTAGNTC	CCCNCAAGT	CNCNCNCTA	360
AACTCANCCN	NATTACNCGC	TTCNTGAGTA	TCACTCCCCG	AATCTCACCC	TACTCAACTC	420
AAAAANATCN	GATACAAAAT	AATNCAAGCC	TGNTTATNAC	ACTNTGACTG	GGTCTCTATT	480
TTAGNGGTCC	NTNAANCNTC	CTAATACTTC	CAGTCTNCCT	TNCACCAATT	CCNAANGGCT	540
CTTTCNGACA	GCATNTTTTG	GTCCTCCTTAN	NGAATTGCC	TTCNTNGAAC	600	
GGGCTCCTCT	TTTCCTTCGG	TTANCTGGN	TTCNNCCGGC	CAGTTATTAT	TTCCCNTTTT	660
AAATTCTNCC	CNTTANTTT	TGGCCTTCNA	AACCCCCGGC	CTTGAAAACG	CCCCCTGGT	720
AAAAGGTTGT	TTTGANAAAA	TTTTTGTGTTT	GTTCC			755

## (2) INFORMATION FOR SEQ ID NO:22:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 849 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TTTTTTTTTT	TTTTTANGTG	TNGTCGTGCA	GGTAGAGGCT	TACTACAANT	GTGAANACGT	60
ACGCTNGGAN	TAANGCGACC	CGANTTCTAG	GANNCCNCCCT	AAAATCANAC	TGTGAAGATN	120
ATCCTGNNA	CGGAANGGTC	ACCGGNNGAT	NNTGCTAGGG	TGNCCNCTCC	CANNNCNTTN	180
CATAACTCNG	NGGCCCTGCC	CACCACCTTC	GGCGGCCNG	NGNCCGGGCC	CGGGTCATTN	240
GNNTTAACCN	CACTNNGCNA	NCGGTTTCCN	NCCCCNNCNG	ACCCNGGCAG	TCCGGGGTNC	300
TCTGTCTTCC	CCTGNAGNCN	ANAAAANTGGG	CCNCGGNCCC	CTTTACCCCT	NNACAAGCCA	360
CNGCCNTCTA	NCCNCNGCCC	CCCCTCCANT	NNGGGGACT	GCCNANNGCT	CCGTTNCTNG	420
NNACCCCN	GGGTNCCTCG	GTTGTCGANT	CNACCGNANG	CCANGGATTG	CNAAGGAAGG	480
TGCGTTNTTG	GCCCCTACCC	TTCGCTNCGG	NNCACCCCTC	CCGACNANGA	NCCGCTCCCG	540
CNCNNCGNNG	CCTCNCTCG	CAACACCCGC	NCTCNCNGT	NCGGNNNNCCC	CCCCACCCGC	600
NCCCTCNCNC	NGNCGNANCN	CTCCNCCNCC	GTCTCANNCA	CCACCCCCGCC	CCGCCAGGCC	660
NTCANCCACN	GGNNGACNNG	NAGCNCNNTC	GCNCCGCGCN	GCNCNCNCCT	CGCCNCNGAA	720
CTNCNTCNGG	CCANTNNGCG	TCAANCCNA	CNAACGCCG	CTGCGCGGCC	CGNAGCGNCC	780
NCCCTCNCGA	GTCCTCCCGN	CTTCCNACCC	ANGNNTTCCN	CGAGGACACN	NNACCCCGCC	840
NNCANGCGG						849

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 872 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GCGCAAACTA	TACTTCGCTC	GNACTCGTGC	GCCTCGCTNC	TCTTTTCCTC	CGCAACCATG	60
TCTGACNANC	CCGATTNGGC	NGATATCNAN	AAGNTCGANC	AGTCCAAACT	GANTAACACA	120
CACACNCNAN	AGANAAATCC	NTCTGCCTTCC	ANAGTANACN	ATTGAACNNG	AGAACCAANGC	180
NGGCGAATCG	TAATNAGGCG	TGCGCCGCCA	ATNTGTCNCC	GTTTATTNTN	CCAGCNCNC	240
CTNCCNACCC	TACNTCTTCN	NAGCTGTCNN	ACCCCTNGTN	CGNACCCCCC	NAGGTCGGGA	300
TCGGGTTTNN	NNTGACCGNG	CNNCCCTCC	CCCCNTCCAT	NACGANCCNC	CCGCACCAACC	360
NANNGCNCGC	NCCCCGNNCT	CTTCGCCNCC	CTGTCCNTN	CCCCGTNGC	CTGGCNCNGN	420
ACCGCATTGA	CCCTCGCCNN	CTNCNNGAAA	NCGNANACGT	CCGGGTTGNN	ANNANCCTG	480
TGGGNNNGCG	TCTGCNCNGC	GTTCTTCCN	NCNNCTTCCA	CCATCTTCNT	TACNGGGTCT	540
CCNCGCCNTC	TCNNNCACNC	CCTGGGACGC	TNTCCTNTGC	CCCCCTTNAC	TCCCCCCCCTT	600
CGNCGTGNCC	CGNCCCCACC	NTCATTTNCA	NACGNTCTTC	ACAANNNCCT	GGNTNNCTCC	660
CNANCNGNCN	GTCANCCNAG	GGAGGGNGG	GGNNCCNNTG	NTTGACGTTG	NGGNGANGTC	720
CGAANANTCC	TCNCCNTCAN	CNCTACCCCT	CGGGCGNNCT	CTCNGTTNCC	AACTTANCAA	780
NTCTCCCCCG	NGNGCNCNTC	TCAGCCTCNC	CCNCCCCNCT	CTCTGCANTG	TNCTCTGCTC	840
TNACCNNTAC	GANTNTTCGN	CNCCCTCTT	CC			872

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 815 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GCATGCAAGC TTGAGTATTCTATAGNGTCA CCTAAATANC TTGGCNTAAT CATGGTCNTA	60
NCTGNCTTCC TGTGTCAAAT GTATACNAAN TANATATGAA TCTNATNTGA CAAGANNGTA	120
TCNTNCATTA GTAAACAANTG TNNTGTCCAT CCTGTCNGAN CANATTCCA TNNATTNCGN	180
CGCATTNCNC GCNCANTATN TAATNGGAA NTCNNNTNNN NCACCCNNCAT CTATCNTNCC	240
GCNCCCTGAC TGGNAGAGAT GGATNANTTC TNNTNTGACC NACATGTTCA TCTTGGATTN	300
AANANCCCCC CGCNGNCCAC CGGTTNGNNG CNAGCCNNTC CCAAGACCTC CTGTGGAGGT	360
AACCTGCGTC AGANNCATCA AACNTGGAA ACCCGCNCC ANGTTNNAAGT NGNNNCANAN	420
GATCCCGTCC AGGNTTNAACC ATCCCTTCAGCAGCCCCCT TTNGTGCCTT ANAGNGNAGC	480
GTGTCCNANC CNCTCAACAT GANACGCGCC AGNCCANCCG CAATTNGGCA CAATGTCGNC	540
GAACCCCCCTA GGGGGANTNA TNCAAANCCC CAGGATTGTC CNCNCANGAA ATCCCNANC	600
CCCNCCCTAC CCNNCTTGG GACNGTGACC AANTCCCGA GTNCCAGTCC GGCCNGNCTC	660
CCCCACCGGT NNCCNTGGGG GGGTGAANCT CNGNNTCANC CNGNCAGGG NTCGNAAGGA	720
ACCGGNCTN GGNCGAANNG ANCNCNTNGA AGNGCCNCNT CGTATAACCC CCCCTCNCCA	780
NCCNACNGNT AGNTCCCCCCC CNGGGTNCGG AANGG	815

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 775 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CCGAGATGTC TCGCTCCGTG GCCTTAGCTG TGCTCGCGCT ACTCTCTCTT TCTGGCCTGG	60
AGGCTATCCA GCGTACTCCA AAGATTCAAGG TTTACTCAAG TCATCCAGCA GAGAATGGAA	120
AGTCAAATTTC CCTGAATTGCTATGTGTCGGTTTCATCC ATCCGACATT GAANTTGACT	180
TACTGAAGAA TGGANAGAGA ATTGAAAAAG TGGAGCATTC AGACTTGTCTTTCAGCAAGG	240
ACTGGTCTTT CTATCTCNTG TACTACACTG AATTCAACCC CACTGAAAAA GATGAGTATG	300
CCTGCCGTGT GAACCATGTG ACTTTGTACAGCAGAT AGTTAAGTGG GATCGAGACA	360
TGTAAGCAGN CNNCATGGAA GTTGAAGAT GCCGCATTG GATTGGATGA ATTCCAATT	420
CTGCTTGCTT GCNTTTAAT ANTGATATGC NTATACACCC TACCCCTTAT GNCCCCAAAT	480
TGTAGGGGTT ACATNANTGT TCNCNTNGGA CATGATCTTC CTTTATAANT CCNCCNTTCG	540
AATTGCCCGT CNCCNGTTN NGAATGTTTC CNNAACCACG GTTGGCTCCC CCAGGTCNCC	600
TCTTACGGAA GGGCTGGGC CNCTTNCAA GTTGGGGGA ACCNAAAATT TCNCTNTGC	660
CCNCCCNCA CNNTCTTGNG NNCNCANTTT GGAACCCCTTC CNATTCCCCCT TGGCCTCNNA	720
NCCTTNNCTA ANAAAACCTTAAANCGTNGC NAAANNTTN ACTTCCCCCCC TTACC	775

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ANATTANTAC AGTGTAATCT TTTCCCAGAG GTGTGTANAG GGAACGGGGC CTAGAGGCAT	60
CCCANAGATA NCTTATANCA ACAGTGCTTT GACCAAGAGC TGCTGGGCAC ATTTCTGCA	120
AAAAAGGTGG CGGTCCCCAT CACTCCTCCT CTCCCATAGC CATCCCAGAG GGGTGAGTAG	180
CCATCANGCC TTCGGTGGGA GGGAGTCANG GAAACAACAN ACCACAGAGC ANACAGACCA	240
NTGATGACCA TGGGCGGGAG CGAGCCTCTT CCCTGNACCG GGGTGGCANA NGANAGCCTA	300
NCTGAGGGGT CACACTATAA ACGTTAACGA CCNAGATNAN CACCTGCTTC AAGTGCACCC	360
TTCCTACCTG ACNACCAGNG ACCNNNAACT GCNGCCTGGG GACAGCCTG GGANCAGCTA	420
ACNNAGCACT CACCTGCCCC CCCATGGCCG TNCGCNTCCC TGTCCTGNC AAGGGAAGCT	480
CCCTGTTGGA ATTNCGGGA NACCAAGGGA NCCCCCTCCT CCANCTGTGA AGGAAAAANN	540
GATGGAATT TNCCTCTCG GCCNNTCCCC TCTTCCTTTA CACGCCCCCT NNTACTCNTC	600
TCCCTCTNTT NTCCTGNNCNC ACTTTTNACC CCNNNATTTC CCTTNATTGA TCGGANCTN	660
GANATTCCAC TNNGCCTNC CNTCNATCNG NAANACNAAA NACTNTCTNA CCCNGGGAT	720
GGGNNCCTCG NTCATCCTCT CTTTTTCNT ACCNCCNTT CTTGCCTCT CCTTNGATCA	780
TCCAACCNTC GNTGGCCNTN CCCCCCNNN TCCTTTNCCC	820

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 818 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TCTGGGTGAT GGCCTCTTCC TCCTCAGGGA CCTCTGACTG CTCTGGCCA AAGAATCTCT	60
TGTTTCTTCT CCGAGCCCCA GGCAGCGGTG ATTCAAGCCCT GCCCAACCTG ATTCTGATGA	120
CTGCGGATGC TGTGACGGAC CCAAGGGGCA AATAGGGTCC CAGGGTCCAG GGAGGGCGC	180
CTGCTGAGCA CTTCCGCCCC TCACCCCTGCC CAGCCCCCTGC CATGAGCTCT GGGCTGGTC	240
TCCGCCTCCA GGGTTCTGCT CTTCCANGCA NGCCANCAAG TGGCGCTGGG CCACACTGGC	300
TTCTTCCCTGC CCCNTCCCTG GCTCTGANTC TCTGTCTTCC TGTCCTGTGC ANGCNCCTTG	360
GATCTCAGTT TCCCTCNCTC ANNGAACTCT GTTTCTGANN TCTTCANTTA ACTNTGANNT	420
TATNACCNAN TGGNCTGTNC TGTCCNACTT TAATGGGCCN GACCGGCTAA TCCCTCCCTC	480
NCTCCCTTCC ANTTCCNNNA ACCNGCTTNC CNTCNCTCTCC CCNTANCCCG CCNGGAANC	540
CTCCTTGCC CTNACCANGG GCCNNNACCG CCCNTNNCTN GGGGGGCNNG GTNNCTNCNC	600
CTGNTNNNNCC CNCTCNNTN TNCCCTGTC CNNCNCNGCN NNGCANNNTTC NCNGTCCNN	660
TNNCTCTTCN NGTNTCGNAA NGNTCNCNTN TNNNNNGNCN NGNTNNNTNCN TCCCTCTCNC	720
CNNNTGNANG TNNTTNNNNC NCNGNNCCCC NNNNCNNNNN NGNNNNNTNNN TCTNCNCNGC	780
CCNNNCCCCC NGNATTAAGG CCTCCNNCTC CGGGCCNC	818

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 731 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

## (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGGAAGGGCG GAGGGATATT GTANGGGATT GAGGGATAGG AGNATAANGG GGGAGGTGTG	60
TCCCAACATG ANGGTGNNGT TCTCTTTGA ANGAGGGTTG NGTTTTANN CCNGGTGGGT	120
GATTNAACCC CATTGTATGG AGNNAAGGN TTTNAGGGAT TTTTCGGCTC TTATCACTAT	180
NTANATTCCCT GTNAATCGGA AAATNATNTT TCNNCNGGAA AATNTTGCTC CCATCCGNA	240
ATTNCTCCCG GGTÄGTGCAT NTTNGGGGGN CNGCCANGTT TCCCAGGCTG CTANAATCGT	300
ACTAAAGNTT NAAGTGGGAN TNCAAATGAA AACCTNNCAC AGAGNATCCN TACCCGACTG	360
TNNNTTNCCCT TCGCCCTNTG ACTCTGCNG AGCCCAATAC CCNNNGNAT GTCNCCNGN	420
NNNGCGNCNC TGAAANNNNC TCGNGGCTNN GANCATCANG GGGTTTCGCA TCAAAAGCNN	480
CGTTTCNCAT NAAGGCACTT TNGCCTCATC CAACCNCCTNG CCCTCNCNNCA TTNNGCCGTC	540
NGGTTCNCCCT ACGCTNNTNG CNCCTNNNTN GANATTTCNC CCGCCTNGGG NAANCCTCCT	600
GNAATGGGTA GGGNCTTNTC TTTTNACCCN GNNGGTNTACT AATCNNTNC ACGCNTNCTT	660
TCTCNACCCCC CCCCTTTT CAATCCCANC GGCNAATGGG GTCTCCCCNN CGANGGGGG	720
NNNCCCCANNC C	731

## (2) INFORMATION FOR SEQ ID NO:29:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ACTAGTCCAG TGTGGTGGAA TTCCATTGTG TTGGGGNCNC TTCTATGANT ANTNTTAGAT	60
CGCTCANACC TCACANCCTC CCNACNANGC CTATAANGAA NANNAATAGA NCTGTNCNNNT	120
ATNTNTACNC TCATANNCCCT CNNNACCCAC TCCCTCTTAA CCCNTACTGT GCCTATNGCN	180
TNNCTANTCT NTGCCGCCTN CNANCCACCN GTGGGCCNAC CNCNNGNATT CTCNATCTCC	240
TCNCCATNTN GCCTANANTA NGTNCATACC CTATACCTAC NCCAATGCTA NNNCTAANCN	300
TCCATNANTT ANNNTAACTA CCACTGACNT NGACTTCNC ATNANCTCCT AATTTGAATC	360
TAATCTGACT CCCACNGCCT ANNNATTAGC ANCNTCCCCC NACNATNTCT CAACCAAATC	420
NTCAACAACC TATCTANCTG TTCNCCAACC NTTNCCTCCG ATCCCCNNAC AACCCCCCTC	480
CCAAATACCC NCCACCTGAC NCCTAACCCN CACCATCCCC GCAAGCCNAN GGNCAATTAN	540
CCACTGGAAT CACNATNGGA NAAAAAAAAC CCNAACTCTC TANCNCNNAT CTCCCTAANA	600
ATNCTCCTN NAATTACTN NCANTNCCAT CAANCCACN TGAAACNNAA CCCCTGTTTT	660
TANATCCCTT CTTTCGAAAA CCNACCCCTT ANNNCCAAC CTTTNGGGCC CCCCCNCTNC	720
CCNAATGAAG GNCNCCAAAT CNANGAAACG NCCNTGAAAA ANCNAAGGCNA ANANNNTCCG	780
CANATCCTAT CCCTTANTTN GGGGNCCCTT NCCCNGGGCC CC	822

## (2) INFORMATION FOR SEQ ID NO:30:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 787 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CGGCCGCCTG	CTCTGGCACA	TGCCTCCTGA	ATGGCATCAA	AAGTGATGGA	CTGCCATTG	60
CTAGAGAAGA	CCTTCTCTCC	TACTGTCATT	ATGGAGCCCT	GCAGACTGAG	GGCTCCCTT	120
GTCTGCAGGA	TTTGATGTCT	GAAGTCGTGG	AGTGTGGCTT	GGAGCTCCTC	ATCTACATNA	180
GCTGGAAGCC	CTGGAGGGCC	TCTCTCGCCA	GCCTCCCCCT	TCTCTCCACG	CTCTCCANGG	240
ACACCAGGGG	CTCCAGGCAG	CCCATTATTG	CCAGNANGAC	ATGGTGTTC	TCCACGGGA	300
CCCATGGGGC	CTGNAAGGCC	AGGGTCTCCT	TTGACACCAT	CTCTCCCGTC	CTGCCCTGGCA	360
GGCCGTGGGA	TCCACTANTT	CTANAACGGN	CGCCACCNCG	GTGGGAGCTC	CAGCTTTGT	420
TCCCTTAAT	GAAGGTTAAT	TGCNCGCTTG	GCGTAATCAT	NGGTCANAAC	TNTTCCCTGT	480
GTGAAATTGT	TTNTCCCCTC	NCNATTCCNC	NCNACATACN	AACCCGGAAN	CATAAAGTGT	540
TAAAGCCTGG	GGGTNGCCTN	NNGAATNAAC	TNAACTCAAT	TAATTGCGTT	GGCTCATGGC	600
CCGTTTCCN	TCNGGAAAAA	CTGTCNTCCC	CTGCNTNNNT	GAATCGGCCA	CCCCCNGGG	660
AAAAGCGGTT	TGCNTTTNG	GGGGNTCCCT	CCNCTCCCC	CCTCNCTAAN	CCCTNCGCCT	720
CGGTCGTTNC	NGGTNGCGGG	GAANGGGNAT	NNNCTCCNC	NAAGGGGGNG	AGNNNGNTAT	780
CCCCAAA						787

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TTTTTTTTTT	TTTTTTTGGC	GATGCTACTG	TTTAATTGCA	GGAGGGGGGG	GTGTGTGTAC	60
CATGTACCAAG	GGCTATTAGA	AGCAAGAAGG	AAGGAGGGAG	GGCAGAGCGC	CCTGCTGAGC	120
AACAAAGGAC	TCCTGCAGCC	TTCTCTGTCT	GTCTCTTGGC	GCAGGCACAT	GGGGAGGCCT	180
CCCGCAGGGT	GGGGGCCACC	AGTCCAGGGG	TGGGAGCACT	ACANGGGTG	GGAGTGGGTG	240
GTGGCTGGTN	CNAATGGCCT	GNACANATC	CCTACGGATT	TTGACACCTG	GATTTCACCA	300
GGGGACCTTC	TGTTCTCCC	NGGNAACTTC	NTNNATCTCN	AAAGAACACA	ACTGTTCTT	360
CNGCANTTCT	GGCTGTTCAT	GGAAAGCACA	GGTGTCCNAT	TTNGGCTGGG	ACTTGGTACA	420
TATGGTTCCG	GCCCACCTCT	CCNCNTCAAN	AAGTAATTCA	CCCCCCCCCN	CCNTCTNTTG	480
CCTGGGCCCT	TAANTACCCA	CACCGGAAC	CANTTANTTA	TTCATCTTNG	GNTGGGCTTG	540
NTNNATCCCN	CCTGAANGCG	CCAAGTTGAA	AGGCCACGCC	GTNCCCNCTC	CCCATAGNAN	600
NTTTTNNCCT	CANCTAATGC	CCCCCNGGC	AACNATCCAA	TCCCCCCCCCN	TGGGGGCC	660
AGCCCANGGC	CCCCGNCTCG	GGNNNCNGN	CNCGNANTCC	CCAGGNTCTC	CCANTCNGNC	720
CCNNNGCNCC	CCCGCACGCA	GAACANAAGG	NTNGAGCCNC	CGCANNNNNN	NGGTNNCNAC	780
CTCGCCCCCCC	CCNNCGNNNG					799

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	60
TTTTNCCNAG	GGCAGGTTA	TGACAACT	CNCGGACAC	AANCAGGCTG	GGGACAGGAC	120
GGCAACAGGC	TCCGGCGCG	CGGGCGGCGG	CCCTACCTGC	GGTACCAAAT	NTGCAGCCTC	180
CGCTCCCGCT	TGATNTTCCT	CTGCAGCTGC	AGGATGCCNT	AAAACAGGGC	CTCGGCCNTN	240
GGTGGGCACC	CTGGGATTTN	AATTCCACG	GGCACAAATGC	GGTCGCANCC	CCTCACCAACC	300
NATTAGGAAT	AGTGGTNTTA	CCNCNCNC	TTGGCNCACT	CCCCNTGGAA	ACCACTTNTC	360
GGGGCTCCGG	CATCTGGTCT	AAACCTTGC	AAACNTGGG	GCCCTTCTTT	TGGTTANTNT	420
NCCNGCCACA	ATCATNACTC	AGACTGGCNC	GGGCTGGCCC	AAAAAAANCN	CCCCAAAACC	480
GGNCCATGTC	TTNNCGGGGT	TGCTGCNATN	TNCATCACCT	CCCGGGCNCA	NCAGGNCAAC	540
CCAAAAGTTC	TTGNGGCCN	AAAAAAANC	CCGGGGGNC	CCAGTTCAA	AAAAGTCATC	600
CCCCCTGGCC	CCCAAATCCT	CCCCCGNTT	NCTGGGTTG	GGAACCCACG	CCTCTNNCTT	660
TGGNNNGCAA	GNTGGNTCCC	CTTCGGGCC	CCCGGTGGGC	CONNCTCTAA	NGAAAACNCC	720
NTCCTNNNCA	CCATCCCCC	NNGNNAACNC	TANCAANGNA	TCCCTTTTTT	TANAAACGGG	780
CCCCCCNCG						789

## (2) INFORMATION FOR SEQ ID NO:33:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 793 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GACAGAACAT	GTTGGATGGT	GGAGCACCTT	TCTATACGAC	TTACAGGACA	GCAGATGGG	60
AATTCAATGGC	TGTTGGAGCA	ATANAACCC	AGTTCTACGA	GCTGCTGATC	AAAGGACTTG	120
GAATCAAAGTC	TGATGAACCT	CCCAATCAGA	TGAGCATGGA	TGATTGGCCA	GAAATGAANA	180
AGAAGTTGC	AGATGTATTT	GCAAAGAAGA	CGAACGGCAGA	GTGGTGTCAA	ATCTTGACG	240
GCACAGATGC	CTGTGTGACT	CCGGTTCTGA	CTTTGAGGA	GGTTGTTCAT	CATGATCACA	300
ACAANGAACG	GGGCTCGTT	ATCACCANTG	AGGAGCAGGA	CGTGAGCCCC	CGCCCTGCAC	360
CTCTGCTGTT	AAACACCCCA	GCCATCCCTT	CTTCAAAAG	GGATCCACTA	CTTCTAGAGC	420
GGNCGCCACC	GCGGTGGAGC	TCCAGCTTT	GTTCCCTTTA	GTGAGGGTTA	ATTGCGCGCT	480
TGGCGTAATC	ATGGTCATAN	CTGTTTCTG	TGTGAAATTG	TTATCCGCTC	ACAATTCCAC	540
ACAACATACG	ANCCGGAAGC	ATNAAATTNT	AAAGCCTGGN	GGTNGCCTAA	TGANTGAACT	600
NACTCACATT	AATTGGCTTT	GCGCTCACTG	CCCGCTTCC	AGTCCGGAAA	ACCTGTCCTT	660
GCCAGCTGCC	NTTAATGAAT	CNGGCCACCC	CCCGGGGAAA	AGGCNGTTG	CTTNTTGGGG	720
CGCNCTTCCC	GCTTCTCGC	TTCTGAANT	CCTTCCCCCC	GGTCTTTCGG	CTTGCGGCNA	780
ACGGTATCNA	CCT					793

## (2) INFORMATION FOR SEQ ID NO:34:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 756 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCCCGCGACCG	GCATGTACGA	GCAACTCAAG	GGCGAGTGGGA	ACCGTAAAAG	CCCCAATCTT	60
ANCAAGTCCG	GGGAANAGCT	GGGTCGACTC	AAGCTAGTTC	TTCTGGAGCT	CAACTTCTTG	120
CCAACCACAG	GGACCAAGCT	GACCAAACAG	CAGCTAATTG	TGGCCCGTGA	CATACTGGAG	180
ATCGGGGCC	AATGGAGCAT	CCTACGCAAN	GACATCCCCT	CCTTCGAGCG	CTACATGGCC	240
CAGCTCAAAT	GCTACTACTT	TGATTACAAN	GAGCAGCTCC	CCGAGTCAGC	CTATATGCAC	300
CAGCTCTTGG	GCCTCAACCT	CCTCTTCCCTG	CTGTCCTTGA	ACCGGGTGGC	TGANTNCCAC	360
ACGGANTTGG	ANCGGCTGCC	TGCCCAANGA	CATACANACC	AATGTCTACA	TCNACCACCA	420
GTGTCCTGGA	GCAAACTGA	TGGANGGCAG	CTACCNAAA	GTNTTCCCTGG	CCNAGGGTAA	480
CATCCCCCGC	CGAGAGCTAC	ACCTTCTTCA	TTGACATCCT	GCTCGACACT	ATCAGGGATG	540
AAAATCGCNG	GGTTGCTCCA	GAAAGGCTNC	AANAANATCC	TTTCNCTGA	AGGCCCCGG	600
ATNCNCTAGT	NCTAGAATCG	GCCC GCCATC	CGGGTGGANC	CTCCAACCTT	TCGTTNCCCT	660
TTACTGAGGG	TTNATTGCCG	CCCTTGGCGT	TATCATGGTC	ACNCCNGTTN	CCTGTGTTGA	720
AATTNTAAC	CCCCACAAT	TCCACGCCNA	CATTNG			756

## (2) INFORMATION FOR SEQ ID NO:35:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGGGATCTCT	ANATCNACCT	GNATGCATGG	TTGTCGGTGT	GGTCGCTGTC	GATGAANATG	60
AACAGGATCT	TGCCCTTGAA	GCTCTCGGCT	GCTGTNTTTA	AGTTGCTCAG	TCTGCCGTCA	120
TAGTCAGACA	CNCTCTGGG	CAAAAAACAN	CAGGATNTGA	GTCTTGATTT	CACCTCCAAT	180
AATCTTCNGG	GCTGTCTGCT	CGGTGAACTC	GATGACNANG	GGCAGCTGGT	TGTGTNTGAT	240
AAANTCCANC	ANGTTCTCCT	TGGTGACCTC	CCCTTCAAAG	TTGTTCCGGC	CTTCATCAA	300
CTTCTNNAAN	ANGANNANCC	CANCTTTGTC	GAGCTGGNAT	TTGGANAACA	CGTCACTGTT	360
GGAAACTGAT	CCCAAATGGT	ATGTCATCCA	TCGCTCTGC	TGCCTGCAA	AAACTTGCTT	420
GGCNCAAATC	CGACTCCCCN	TCCCTGAAAG	AAGCCNATCA	CACCCCCCTC	CCTGGACTCC	480
NNCAANGACT	CTNCCGCTNC	CCCNCTCCNN	CAGGGTTGGT	GGCANNCCGG	GCCCNTGCGC	540
TTCTTCAGCC	AGTTCACNAT	NTTCATCAGC	CCCTCTGCCA	GCTGTTNTAT	TCCTTGGGG	600
GGAANCCGTC	TCTCCCTTCC	GAANNAACT	TTGACCGTNG	GAATAGCCGC	GCNTCNCNT	660
ACNTNCTGGG	CCGGGTTCAA	ANTCCCTCCN	TTGNCNNTCN	CCTCGGGCCA	TTCTGGATTT	720
NCCNAACTTT	TTCCCTCCCC	CNCCCCNCGG	NGTTGGNTT	TTTCATNGGG	CCCCAACTCT	780
GCTNTTGGCC	ANTCCCCTGG	GGGCNTNTAN	CNCCCCCTNT	GGTCCCNNTNG	GGCC	834

## (2) INFORMATION FOR SEQ ID NO:36:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CGGNCGCTTT	CCNGCCGCGC	CCCGTTCCA	TGACNAAGGC	TCCCTTCANG	TTAAATACNN	60
CCTAGNAAAC	ATTAATGGGT	TGCTCTACTA	ATACATCATA	CNAACCAGTA	AGCCTGCCA	120
NAACGCCAAC	TCAGGCCATT	CCTACCAAAG	GAAGAAAGGC	TGGTCTCTCC	ACCCCTGTA	180
GGAAAGGCCT	GCCTTGTAAAG	ACACCACAAT	NCGGCTGAAT	CTNAAGTCTT	GTGTTTACT	240
AATGGAAAAA	AAAAATAAAC	AANAGGTTT	GTTCTCATGG	CTGCCCCACCG	CAGCCTGGCA	300
CTAAAACANC	CCAGCGCTCA	CTTCTGCTTG	GANAAATATT	CTTGCTCTT	TTGGACATCA	360
GGCTTGATGG	TATCACTGCC	ACNTTTCCAC	CCAGCTGGGC	NCCCTTCCCC	CATNTTGTC	420
ANTGANCTGG	AAGGCCTGAA	NCTTAGTCTC	CAAAAGTCTC	NGCCCACAAG	ACCGGCCACC	480
AGGGGANGTC	NTTNCAGTG	GATCTGCCAA	ANANTACCCN	TATCATCNNT	GAATAAAAAG	540
GCCCCCTGAAC	GANATGCTTC	CANCANCCTT	TAAGACCCAT	AATCCTNGAA	CCATGGTGCC	600
CTTCCGGTCT	GATCCNAAAG	GAATGTTCCCT	GGGTCCCANT	CCCTCCTTTG	TTNCTTACGT	660
TGTNTTGGAC	CCNTGCTNGN	ATNACCCAAN	TGANATCCCC	NGAAGCACCC	TNCCCCTGGC	720
ATTIGANTTT	CNTAAATTCT	CTGCCCTACN	NCTGAAAGCA	CNATTCCCTN	GGCNCCNAAN	780
GGNGAACTCA	AGAAGGTCTN	NGAAAAACCA	CNCN			814

## (2) INFORMATION FOR SEQ ID NO:37:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 760 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GCATGCTGCT	CTTCCTCAA	GTGTTCTTG	TTGCCATAAC	AACCACCATA	GGTAAAGCGG	60
GGCAGTGT	CGCTGAAGGG	GTGTTAGTAC	CAGCGCGGA	TGCTCTCCTT	GCAGAGTCCT	120
GTGTCTGGCA	GGTCCACGCA	ATGCCCTTTG	TCACTGGGA	AATGGATGCG	CTGGAGCTCG	180
TCNAANCCAC	TCGTGTATTT	TTCACANGCA	GCCTCCTCCG	AAGCNTCCGG	GCAGTTGGGG	240
GTGTCGTAC	ACTCCACTAA	ACTGTCGATN	CANCAAGCCA	TTGCTGCAGC	GGAACTGGGT	300
GGGCTGACAG	GTGCCAGAAC	ACACTGGATN	GGCCTTCCA	TGGAAGGGCC	TGGGGGAAAT	360
CNCCTNANCC	CAAACCTGCCT	CTCAAAGGCC	ACCTTGACACA	CCCCGACAGG	CTAGAAATGC	420
ACTCTTCTTC	CCAAAGGTAG	TTGTTCTTGT	TGCCCAAGCA	NCCTCCANCA	AACCAAANC	480
TTGCAAAATC	TGCTCCGTGG	GGGTCAATNNN	TACCANGTT	GGGGAAANAA	ACCCGGCNGN	540
GANCCNCCTT	GTGTTGAATGC	NAAGGNAATA	ATCCTCCTGT	CTTGCTTGGG	TGGAANAGCA	600
CAATTGAACT	GTAAACNTTG	GGCCGNGTTC	CNCTNGGGTG	GTCTGAAACT	AATCACCGTC	660
ACTGGAAAAA	GGTANGTGCC	TTCCCTTGAAT	TCCCAAANTT	CCCCTNGNTT	TGGGTNNNTT	720
CTCCTCTNCC	CTAAAAATCG	TNTTCCCCCC	CCNTANGGCG			760

## (2) INFORMATION FOR SEQ ID NO:38:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 724 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TTTTTTTTTT	TTTTTTTTTT	TTTTTAAAAA	CCCCCTCCAT	TGAATGAAAA	60
CTTCCNAAAT	TGTCCAACCC	CCTCNCCAA	ATNNCCATT	CGGGGGGGGG	120

CAAATTAATT TTGGANTTA AATTAATNT TNATTNGGG AANAANCAA ATGTNAAGAA	180
AATTTAACCC ATTATNAACT TAAATNCCTN GAAACCCNTG GNTTCCAAAATTTTAACC	240
CTTAAATCCC TCCGAAATTG NTAANGAAA ACCAAATTCTN CCTAAGGCTN TTTGAAGGTT	300
NGATTTAACC CCCCTTNANT TNTTTNACC CNNGNCTNAA NTATTTNGNT TCCGGTGT	360
TCCNTNTAAN CNTNGGTAAAC TCCCGNTAAT GAANNCCCT AANCCAATTA AACCGAATT	420
TTTTGAATT GGAAATTCCN NGGGAATTNA CGGGGGTTT TCCCTTTGG GGGCCATNCC	480
CCCNCTTCG GGGTTGGGN NTAGGTTGAA TTTTNANG NCCCAAAAAA NCCCCCAANA	540
AAAAAAACTCC CAAGNNTAA TTNGAATNTC CCCCTTCCCA GGCCTTTGG GAAAGGNGGG	600
TTTNTGGGGG CCNNGGANTT CNTTCCCCN TTNCCNCCCC CCCCCCNGGT AAANGTTAT	660
NGNNNTTGGT TTTGGGCC CTTNANGGAC CTTCCGGATN GAAATTAAAT CCCCAGGNCG	720
GCCG	724

## (2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TTTTTTTTTT TTTTTCTTTG CTCACATTAA ATTTTTATTT TGATTTTTTT TAATGCTGCA	60
CAACACAAATA TTTATTCAT TTGTTCTTT TATTTCATTT TATTTGTTTG CTGCTGCTGT	120
TTTATTTATT TTTACTGAAA GTGAGAGGGA ACTTTTGTTGG CCTTTTTTCC TTTTTCTGTA	180
GGCCGCCTTA AGCTTTCTAA ATTGGAACA TCTAAGCAAG CTGAANGAA AAGGGGGTTT	240
CGAAAATCA CTCGGGGAA NGGAAAGGTT GCTTGTAA TCATGCCCTA TGGTGGGTGA	300
TTAACTGCTT GTACAATTAC NTTCACTTT TAATTAATTG TGCTNAANGC TTTAATTANA	360
CTTGGGGGTT CCCTCCCCAN ACCAACCCCCN CTGACAAAAA GTGCCNGCCC TCAAATNATG	420
TCCCGGCNNT CNTTGAAACA CACNGCNGAA NGTTCTCATT NTCCCCNCNC CAGGTNAAAA	480
TGAAGGGTTA CCATNTTAA CNCCACCTCC ACNTGGCANN GCCTGAATCC TCNAAAANCN	540
CCCTCAANCN AATTNCTNNG CCCCGGTNC GCNTNNGTCC CNCCCNGCT CCGGGAANTN	600
CACCCCCNGA ANNCNNTNNC NAACNAAATT CCGAAAATAT TCCCNNTCNC TCAATTCCCC	660
CNNAGACTNT CCTCENNAN CNCAATTTC TTTTNNTCAC GAACNCGNNC CNNAAAATGN	720
NNNNNCNCCTC CNCTNGTCCN NAATCNCAN C	751

## (2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 753 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GTGGTATTTT CTGTAAGATC AGGTGTTCCCT CCCTCGTAGG TTTAGAGGAA ACACCCCTCAT	60
AGATGAAAAC CCCCCCGAGA CAGCAGCACT GCAACTGCCA AGCAGCCGGG GTAGGAGGGG	120
CGCCCTATGC ACAGCTGGGC CCTTGAGACA GCAGGGCTTC GATGTCAGGC TCGATGTCAA	180
TGGTCTGGAA GCGGCGGCTG TACCTGCGTA GGGGCACACC GTCAGGGCCC ACCAGGAAC	240
TCTCAAAGTT CCAGGCAACN TCGTTGCGAC ACACCGGAGA CCAGGTGATN AGCTTGGGT	300

CGGTCTATAAN CGCGGGTGGCG TCGTCGCTGG GAGCTGGCAG GGCCTCCCGC AGGAAGGCNA	360
ATAAAAGGTG CGCCCCCGCA CGGTTCANCT CGCACTTCTC NAANACCATG ANGTTGGGCT	420
CNAACCCACC ACCANNCCGG ACTTCCTTGA NGGAATTCCC AAATCTCTTC GNTCTGGGC	480
TTCTNCTGAT GCCCTANCTG GTTGCCTNGN ATGCCAANCA NCCCCAANCC CCGGGGTCCCT	540
AAANCACCCN CCTCCTCCTT TCATCTGGGT TNTTNCCCC GGACCNNTGGT TCCTCTCAAG	600
GGANCCCATA TCTCNACCAN TACTCACCNT NCCCCCCCNT GNNAACCCANC CTTCTANNGN	660
TTCCCNCCCG NCCTCTGGCC CNTCAAANAN GCTTNACNA CCTGGGTCTG CCTTCCCCCC	720
TNCCCTATCT GNACCCNCN TTTGTCTCAN TNT	753

## (2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 341 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ACTATATCCA TCACAACAGA CATGCTTCAT CCCATAGACT TCTTGACATA GCTTCAAATG	60
AGTGAACCCA TCCTTGATTT ATATACATAT ATGTTCTCAG TATTTTGGGA GCCTTTCCAC	120
TTCTTTAACCTTGTGATT ATGAACACTG AAAATAGGAA TTTGTGAAGA GTTAAAAAGT	180
TATAGCTTGT TTACGTAGTA AGTTTTTGAA GTCTACATTC AATCCAGACA CTTAGTTGAG	240
TGTTAAACTG TGATTTTAA AAAATATCAT TTGAGAATAT TCTTCAGAG GTATTTTCAT	300
TTTACTTT TGATTAATTG TGTTTATAT ATTAGGGTAG T	341

## (2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 101 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ACTTACTGAA TTTAGTTCTG TGCTCTTCCT TATTTAGTGT TGTATCATAA ATACTTGAT	60
GTTCACAAACA TTCTAAATAA ATAATTTCA GTGGCTTCAT A	101

## (2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 305 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ACATCTTGT TACAGTCTAA GATGTGTTCT TAAATCACCA TTCCCTTCCTG GTCCTCACCC	60
TCCAGGGTGG TCTCACACTG TAATTAGAGC TATTGAGGAG TCTTACAGC AAATTAAGAT	120
TCAGATGCCT TGCTAAGTCT AGAGTTCTAG AGTTATGTTT CAGAAAGTCT AAGAAACCCA	180
CCTCTTGAGA GGTCAAGTAA GAGGACTTAA TATTTCATAT CTACAAAATG ACCACAGGAT	240
TGGATACAGA ACGAGAGTTA TCCTGGATAA CTCAGAGCTG AGTACCTGCC CGGGGGCCGC	300
TCGAA	305

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 852 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

ACATAAATAT CAGAGAAAAG TAGTCTTGA AATATTTACG TCCAGGAGTT CTTTGTGTTCT	60
GATTATTG G TGTGTGTTT GGTTTGTGTC CAAAGTATTG GCAGCTTCAG TTTTCATTTT	120
CTCTCCATCC TCGGGCATTTC TTCCCAAATT TATATACCAG TCTTCGTCCA TCCACACGCT	180
CCAGAATTTC TCTTTGTAG TAATATCTCA TAGCTGGCT GAGCTTTCA TAGGTCATGC	240
TGCTGTTGTT CTTCTTTTA CCCCATAGCT GAGCCACTGC CTCTGATTTC AAGAACCTGA	300
AGACGCCCTC AGATCGGTCT TCCCATTGTTA TTAATCCTGG GTTCTTGTCT GGGTTCAAGA	360
GGATGTCGCG GATGAATTCC CATAAGTGAG TCCCTCTCGG GTTGTGCTTT TTGGTGTGGC	420
ACTTGGCAGG GGGTCTTGC TCCCTTTCA TATCAGGTGA CTCTGCAACA GGAAGGTGAC	480
TGGTGGTTGT CATGGAGATC TGAGCCCGGC AGAAAGTTTT GCTGTCCAAC AAATCTACTG	540
TGCTACCAT A GTGGTGTCA TATAAATAGT TCTNGTCTTT CCAGGTGTTC ATGATGGAAG	600
GCTCAGTTTG TTCAGTCTG ACAATGACAT TGTGTGTTGA CTGGAACAGG TCACTACTGC	660
ACTGGCCGTT CCACCTTCAGA TGCTGCAAGT TGCTGTAGAG GAGNTGCCCG GCGTCCCTG	720
CCGCCCGGGT GAACTCCTGC AAACATCATGC TGCAAAGGTG CTCGCCGTTG ATGTCGAAC	780
CNTGGAAAGG GATACAATTG GCATCCAGCT GGTTGGTGTCA CAGGAGGTGA TGGAGCCACT	840
CCCACACCTG GT	852

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

ACAACAGACC CTTGCTCGCT AACGACCTCA TGCTCATCAA GTTGGACGAA TCCGTGTCCG	60
AGTCTGACAC CATCCGGAGC ATCAGCATTG CTTCGCAGTG CCCTACCGCG GGGAACTCTT	120
GCCTCGTTTC TGGCTGGGT CTGCTGGCGA ACGGCAGAAT GCCTACCGTG CTGCAGTGCG	180
TGAACGTGTC GGTGGTGTCT GAGGAGGTCT GCAGTAAGCT CTATGACCCCG CTGT	234

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 590 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ACTTTTTATT TAAATGTTTA TAAGGCAGAT CTATGAGAAT GATAGAAAAC ATGGTGTGTA	60
ATTTGATAGC AATATTTGG AGATTACAGA GTTTTAGTAA TTACCAATTAA CACAGTTAAA	120
AAGAAGATAA TATATTCCAA GCANATACAA AATATCTAA GAAAGATCAA GGCAGGAAAA	180
TGANTATAAC TAATTGACAA TGGAAAATCA ATTTTAATGT GAATTGCACA TTATCCTTTA	240
AAAGCTTTCA AAANAAANAA TTATTGCAGT CTANTTAATT CAAACAGTGT TAAATGGTAT	300
CAGGATAAAN AACTGAAGGG CANAAAGAAAT TAATTTTCAC TTCATGTAAC NCACCCANAT	360
TTACAATGGC TTAAATGCAN GGAAAAAGCA GTGGAAGTAG GGAAGTANTC AAGGTCTTTC	420
TGGTCTCTAA TCTGCCTTAC TCTTTGGGTG TGGCTTGAT CCTCTGGAGA CAGCTGCCAG	480
GGCTCCTGTT ATATCCACAA TCCCAGCAGC AAGATGAAGG GATGAAAAAG GACACATGCT	540
GCCTTCCTTT GAGGAGACTT CATCTCACTG GCCAACACTC AGTCACATGT	590

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 774 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ACAAGGGGGC ATAATGAAGG AGTGGGGANA GATTTAAAG AAGGAAAAAA AACGAGGCC	60
TGAACAGAAT TTTCCTGNAC AACGGGGCTT CAAAATAATT TTCTTGGA GGTTCAAGAC	120

GCTTCACTGC TTGAAACTTA AATGGATGTG GGACANAATT TTCTGTAATG ACCCTGAGGG	180
CATTACAGAC GGGACTCTGG GAGGAAGGAT AAACAGAAAG GGGACAAAGG CTAATCCAA	240
AACATCAAAG AAAGGAAGGT GGCCTACAC CTCCCAGCCT ACACAGTTCT CCAGGGCTCT	300
CCTCATCCCT GGAGGACGAC AGTGGAGGAA CAACTGACCA TGTCAGGAGG CTCCTGTGTG	360
CTGGCTCTG GTCTTCAGCC CCCAGCTCTG GAAGCCCACC CTCTGCTGAT CCTGCCTGGC	420
CCACACTCCT TGAACACACA TCCCCAGGTT ATATTCTGG ACATGGCTGA ACCTCCATT	480
CCTACTTCCG AGATGCCTTG CTCCCTGCAG CCTGTCAAAA TCCCACTCAC CCTCCAAACC	540
ACGGCATGGG AAGCCTTCT GACTTGCTG ATTACTCCAG CATCTTGAA CAATCCCTGA	600
TTCCCCACTC CTTAGAGGCA AGATAGGGTG GTTAAGAGTA GGGCTGGACC ACTTGGAGCC	660
AGGCTGCTGG CTTCAAATTN TGGCTCATTT ACGAGCTATG GGACCTTGGG CAAGTNATCT	720
TCACTTCTAT GGGCNTCATT TTGTTCTACC TGCAAAATGG GGGATAATAA TAGT	774

## (2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CANAAATTGA AATTTTATAA AAAGGCATTT TTCTCTATA TCCATAAAAT GATATAATTT	60
TTGCAANTAT ANAAATGTGT CATAAATTAT AATGTTCTT AATTACAGCT CAACGCAACT	120
TGGT	124

## (2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GCCGATGCTA CTATTTTATT GCAGGAGGTG GGGGTGTTT TATTATTCTC TCAACAGCTT	60
TGTGGCTACA GGTGGTGTCT GACTGCATNA AAAANTTTT TACGGGTGAT TGCAAAAATT	120
TTAGGGCACC CATATCCAA GCANTGT	147

## (2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

ACATTAAATT AATAAAAGGA CTGTTGGGGT TCTGCTAAAA CACATGGCTT GATATATTGC 60  
 ATGGTTTGAG GTTAGGAGGA GTTAGGCATA TGTTTGGGA GAGGGGT 107

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 204 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GTCCTAGGAA GTCTAGGGAA CACACGACTC TGGGGTCACG GGGCCGACAC ACTTGCACGG 60  
 CGGGAAGGAA AGGCAGAGAA GTGACACCGT CAGGGGGAAA TGACAGAAAG GAAAATCAAG 120  
 GCCTTGCAAG GTCAGAAAGG GGACTCAGGG CTTCCACCAC AGCCCTGCCA CACTTGCCCA 180  
 CCTCCCTTTT GGGACCAGCA ATGT 204

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 491 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ACAAAGATAA CATTATCTT ATAACAAAAA TTTGATAGTT TAAAGGTTA GTATTGTGTA 60  
 GGGTATTTTC CAAAAGACTA AAGAGATAAC TCAAGGAAAA AGTTAGAAAT GTATAAAACA 120  
 CCATCAGACA GGTTTTAAA AAACAACATA TTACAAAATT AGACAATCAT CCTTAAAAAA 180  
 AAAACTTCTT GTATCAATT CTTTGTCA AAATGACTGA CTTAANTATT TTTAAATATT 240  
 TCAAAACAC TTCCTCAAAA ATTTCAANA TGGTAGCTT CANATGTNCC CTCAGTCCCA 300  
 ATGTTGCTCA GATAAATAAA TCTCGTGAGA ACTTACCAACC CACCACAAGC TTTCTGGGC 360  
 ATGCAACAGT GTCTTTCTT TNCTTTTCTT TTTTTTTTT TTACAGGCAC AGAAACTCAT 420

CAATTTTATT TGGATAACAA AGGGTCTCCA AATTATATTG AAAAATAAAT CCAAGTTAAT 480  
ATCACTCTTG T 491

## (2) INFORMATION FOR SEQ ID NO:53:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

ACATAATTAA GCAGGGCTAA TTACCATAG ATGCTATTAA TTAANAGGTN TATGATCTGA	60
GTATTAACAG TTGCTGAAGT TTGGTATTAA TATGCAGCAT TTTCTTTTG CTTTGATAAC	120
ACTACAGAAC CCTTAAGGAC ACTGAAAATT AGTAAGTAAA GTTCAGAAC ATTAGCTGCT	180
CAATCAAATC TCTACATAAC ACTATAGTAA TTAAACGTT AAAAAAAAGT GTTGAAATCT	240
GCACTAGTAT ANACCGCTCC TGTCAGGATA ANACTGCTTT GGAACAGAAA GGGAAAANC	300
AGCTTTGANT TTCTTTGTGC TGATANGAGG AAAGGCTGAA TTACCTTGTT GCCTCTCCCT	360
AATGATTGGC AGGTCNGGTA AATNCCAAAA CATATTCCAA CTCAACACTT CTTTCCNCG	420
TANCTTGANT CTGTGTATTC CAGGANCAGG CGGATGGAAT GGGCCAGCCC NCGGATGTT	480
CANT	484

## (2) INFORMATION FOR SEQ ID NO:54:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ACTAAACCTC GTGCTTGTGA ACTCCATACA GAAAACGGTG CCATCCCTGA ACACGGCTGG	60
CCACTGGGTA TACTGCTGAC AACCGCAACA ACAAAAACAC AAATCCTTGG CACTGGCTAG	120
TCTATGTCTT CTCAAGTGCC TTTTTGTTTG T	151

## (2) INFORMATION FOR SEQ ID NO:55:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

ACCTGGCTTG TCTCCGGGTG GTTCCCGGCG CCCCCCACGG TCCCCAGAAC GGACACTTTC	60
GGCCCTCCAGT GGATACTCGA GCCAAAGTGG T	91

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGCGGATGTG CGTTGGTTAT ATACAAATAT GTCATTTAT GTAAGGGACT TGAGTATACT	60
TGGATTTTG GTATCTGTGG GTTGGGGGGA CGGTCCAGGA ACCAATACCC CATGGATACC	120
AAGGGACAAAC TGT	133

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

ACTCTGGAGA ACCTGAGCCG CTGCTCCGCC TCTGGGATGA GGTGATGCAN GCNGTGGCGC	60
GACTGGGAGC TGAGCCCTTC CCTTTGCGCC TGCCTCAGAG GATTGTTGCC GACNTGCANA	120
TCTCANTGGG CTGGATNCAT GCAGGGT	147

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

ACAGGGATAT AGGTTTNAAG TTATTGTNAT TGTAAAATAC ATTGAATTTT CTGTATACTC	60
TGATTACATA CATTATCCT TAAAAAAAGA TGAAATCTT AATTTTTATG CCATCTATTA	120
ATTTACCAAT GAGTTACCTT GTAAATGAGA AGTCATGATA GCACTGAATT TTAACTAGTT	180
TTGACTTCTA AGTTTGGT	198

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

ACAACAAATG GGTTGTGAGG AAGCTTTATC AGCAAAACTG GTGATGGCTA CTGAAAAGAT	60
CCATTGAAAA TTATCATTAA TGATTTTAAA TGACAAGTTA TCAAAAACTC ACTCAATTT	120
CACCTGTGCT AGCTTGCTAA AATGGGAGTT AACTCTAGAG CAAATATAGT ATCTTCTGAA	180
TACAGTCAAT AAATGACAAA GCCAGGGCCT ACAGGTGGTT TCCAGACTTT CCAGACCCAG	240
CAGAAGGAAT CTATTTTATC ACATGGATCT CCGTCTGTGC TCAAAATACC TAATGATATT	300
TTTCGTCTTT ATTGGACTTC TTTGAAGAGT	330

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

ACCGTGGGTG CCTTCTACAT TCCTGACGGC TCCCTCACCA ACATCTGGTT CTACTTCGGC	60
GTCGTGGCT CCTTCCTCTT CATCCTCATC CAGCTGGTGC TGCTCATCGA CTTTGCGCAC	120
TCCTGGAACC AGCGGTGGCT GGGCAAGGCC GAGGAGTGC ATTCCCGTGC CTGGT	175

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 154 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

ACCCCACTTT TCCTCCTGTG AGCAGTCTGG ACTTCTCACT GCTACATGAT GAGGGTGAGT	60
GGTTGTTGCT CTTAACAGT ATCCTCCCCCT TTCCGGATCT GCTGAGCCGG ACAGCAGTGC	120
TGGACTGCAC AGCCCCGGGG CTCCACATTG CTGT	154

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 30 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CGCTCGAGCC CTATAGTGAG TCGTATTAGA	30
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(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 89 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

ACAAGTCATT TCAGCACCCCT TTGCTCTTCA AAACTGACCA TCTTTTATAT TTAATGCTTC	60
CTGTATGAAT AAAAATGGTT ATGTCAAGT	89

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 97 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ACCGGAGTAA CTGAGTCGGG ACGCTGAATC TGAATCCACC AATAAATAAA GGTTCTGCAG	60
AATCAGTGCA TCCAGGATTG GTCCTTGGAT CTGGGGT	97

## (2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 377 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

ACAACAANAA NTCCCTTCTT TAGGCCACTG ATGGAAACCT GGAACCCCCT TTTGATGGCA	60
GCATGGCGTC CTAGGCCCTG ACACAGCGGC TGGGGTTTGG GCTNTCCCAA ACCGCACACC	120
CCAACCCTGG TCTACCCACA NTTCTGGCTA TGGGCTGTCT CTGCCACTGA ACATCAGGGT	180
TCGGTCATAA NATGAAATCC CAANGGGGAC AGAGGTCAGT AGAGGAAGCT CAATGAGAAA	240
GGTGCTGTTT GCTCAGCCAG AAAACAGCTG CCTGGCATTC GCGCTGAAC TATGAACCCG	300
TGGGGGTGAA CTACCCCCAN GAGGAATCAT GCCTGGCGA TGCAANGGTG CCAACAGGAG	360
GGCCGGGAGG AGCATGT	377

## (2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 305 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

ACGCCTTCC CTCAGAATTC AGGGAAGAGA CTGTCGCCTG CCTTCCTCCG TTGTTGCGTG	60
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AGAACCCGTG TGCCCTTCC CACCATATCC ACCCTCGCTC CATCTTGAA CTCAAACACG	120
AGGAACTAAC TGCACCCCTGG TCCTCTCCCC AGTCCCCAGT TCACCCCTCCA TCCCTCACCT	180
TCCCTCCACTC TAAGGGATAT CAACACTGCC CAGCACAGGG GCCCTGAATT TATGTGGTTT	240
TTATATATTT TTTAATAAGA TGCACTTTAT GTCATTTTT AATAAAAGTCT GAAGAATTAC	300
TGTTT	305

## (2) INFORMATION FOR SEQ ID NO:67:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

ACTACACACACA CTCCACTTGC CTTTGTGAGA CACTTTGTCC CAGCACTTTA GGAATGCTGA	60
GGTCGGACCA GCCACATCTC ATGTGCAAGA TTGCCAGCA GACATCAGGT CTGAGAGTTC	120
CCCTTTTAAA AAAGGGGACT TGCTTAAAAA AGAAGTCTAG CCACGATTGT GTAGAGCAGC	180
TGTGCTGTGC TGGAGATTCA CTTTGAGAG AGTTCTCCTC TGAGACCTGA TCTTTAGAGG	240
CTGGGCAGTC TTGCACATGA GATGGGGCTG GTCTGATCTC AGCACTCCTT AGTCTGCTTG	300
CCTCTCCCAG GGCCCCAGCC TGGCACACCC TGCTTACAGG GCACCTCTCAG ATGCCCATAC	360
CATAGTTCT GTGCTAGTGG ACCGT	385

## (2) INFORMATION FOR SEQ ID NO:68:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

ACTTAAACCAAG ATATATTTT ACCCCAGATG GGGATATTCT TTGTAAAAAA TGAAAATAAA	60
GTTCCTTTAA TGG	73

## (2) INFORMATION FOR SEQ ID NO:69:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

ACTAGTCCAG	TGTGGTGGAA	TTCCATTGTG	TTGGGGCTC	TCACCCCTCCT	CTCCTGCAGC	60
TCCAGCTTTG	TGCTCTGCCT	CTGAGGAGAC	CATGGCCAG	CATCTGAGTA	CCCTGCTGCT	120
CCTGCTGGCC	ACCCTAGCTG	TGGCCCTGGC	CTGGAGCCCC	AAGGAGGAGG	ATAGGATAAT	180
CCCGGGTGGC	ATCTATAACG	CAGACCTCAA	TGATGAGTGG	GTACAGCGTG	CCCTTCACCT	240
CGCCATCAGC	GAGTATAACA	AGGCCACCAA	AGATGACTAC	TACAGACGTC	CGCTGCGGGT	300
ACTAAGAGCC	AGGCAACAGA	CCGTTGGGGG	GGTGAATTAC	TTCTTCGACG	TAGAGGTGGG	360
CCGAACCATA	TGTACCAAGT	CCCAGCCAA	CTTGGACACC	TGTGCCTTCC	ATGAACAGCC	420
AGAACTGCAG	AAGAAACAGT	TGTGCTCTTT	CGAGATCTAC	GAAGTTCCCT	GGGGAGAACA	480
GAANGTCCCT	GGGTGAAATC	CAGGTGTCAA	GAAATCCTAN	GGATCTGTTG	CCAGGC	536

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

ATGACCCCTA	ACAGGGGGCC	TCTCAGCCCT	CCTAATGACC	TCCGGCCTAG	CCATGTGATT	60
TCACCTCCAC	TCCATAACGC	TCCTCATACT	AGGCCTACTA	ACCAACACAC	TAACCATATA	120
CCAATGATGG	CGCGATGTAA	CACGAGAAAG	CACATACCAA	GGCCACCACA	CACCACCTGT	180
CCAAAAGGC	CTTCGATACG	GGATAATCCT	ATTTATTACC	TCAGAAGTTT	TTTTCTTCGC	240
AGGGATTTTT	CTGAGCCTTT	TACCACTCCA	GCCTAGCCCC	TACCCCCCAA	CTAGGAGGGC	300
ACTGGCCCCC	AACAGGCATC	ACCCCGCTAA	ATCCCCTAGA	AGTCCCACTC	CTAAACACAT	360
CCGTATTACT	CGCATCAGGA	GTATCAATCA	CCTGAGCTCA	CCATAGTCTA	ATAGAAAACA	420
ACCGAAACCA	AATTATTCAA	AGCACTGCTT	ATTACAATT	TACTGGGTCT	CTATTTT	477

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 533 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

AGAGCTATAG	GTACAGTGTG	ATCTCAGCTT	TGCAAACACA	TTTCTACAT	AGATAGTACT	60
AGGTATTAAT	AGATATGTAA	AGAAAGAAAT	CACACCATTA	ATAATGGTAA	GATTGGTTA	120
TGTGATTTA	GTGGTATTT	TGGCACCCCTT	ATATATGTTT	TCCAAACTTT	CAGCAGTGAT	180
ATTATTTCCA	TAACCTAAAA	AGTGAGTTG	AAAAAGAAAA	TCTCCAGCAA	GCATCTCATT	240
TAAATAAAGG	TTTGTCTACT	TTAAAAATAC	AGCAATATGT	GACTTTTAA	AAAAGCTGTC	300
AAATAGGTGT	GACCCTACTA	ATAATTATTA	GAAATACATT	TAAAAACATC	GAGTACCTCA	360
AGTCAGTTG	CCTTGAAAAA	TATCAAATAT	AACTCTAGA	GAAATGTACA	AAAAAGAATG	420
CTTCGTAATT	TTGGAGTANG	AGGTTCCCTC	CTCAATTG	TATTTTAAA	AAGTACATGG	480
TAAAAAAA	AATTACAAC	AGTATATAAG	GCTGTAAAAT	GAAGAATTCT	GCC	533

## (2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 511 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

TATTACGGAA	AAACACACCA	CATAATTCAA	CTANCAAAGA	ANACTGCTTC	AGGGCGTGTA	60
AAATGAAAGG	CTTCCAGGCA	GTATCTGAT	TAAAGAACAC	AAAAGAGGG	ACAAGGCTAA	120
AAGCCGCAGG	ATGTCTACAC	TATANCAGGC	GCTATTGGG	TTGGCTGGAG	GAGCTGTGGA	180
AAACATGGAN	AGATTGGTGC	TGGANATCGC	CGTGGCTATT	CCTCATTGTT	ATTACANAGT	240
GAGGTTCTCT	GTGTGCCAC	TGTTTGAAA	ACCGTTCTNC	AATAATGATA	GAATAGTACA	300
CACATGAGAA	CTGAAATGGC	CCAAACCCAG	AAAGAAAGCC	CAACTAGATC	CTCAGAAANAC	360
GCTTCTAGGG	ACAATAACCG	ATGAAGAAAA	GATGGCCTCC	TTGTGCCCCC	GTCTGTTATG	420
ATTCTCTCC	ATTGCAGCNA	NAAACCCGTT	CTTCTAAGCA	AACNCAGGTG	ATGATGGCNA	480
AAATACACCC	CCTCTTGAAG	NACCNGGAGG	A			511

## (2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 499 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

CAGTGCCAGC	ACTGGTGCCA	GTACCAAGTAC	CAATAACAGT	GCCAGTGCCA	GTGCCAGCAC	60
CAGTGGTGGC	TTCAGTGCTG	GTGCCAGCCT	GACCGCCACT	CTCACATTG	GGCTCTCGC	120
TGGCCTTGGT	GGAGCTGGTG	CCAGCACCAAG	TGGCAGCTCT	GGTGCCTGTG	GTTCCTCTA	180
CAAGTGAGAT	TTTAGATATT	GTAAATCCTG	CCAGTCTTTC	TCTTCAAGCC	AGGGTGCATC	240

CTCAGAAACC TACTAACAC AGCACTCTAG GCAGCCACTA TCAATCAATT GAAAGTTGACA	300
CTCTGCATTA AATCTATTTG CCATTTCTGA AAAAAAAA AAAAAAAGGG CGGCCGCTCG	360
ANTCTAGAGG GCCCCTTAA ACCCGCTGAT CAGCCTCGAC TGTGCCTTCT ANTTGCCAGC	420
CATCTGTTGT TTGCCCCCTCC CCCGNTGCCT TCCTTGACCC TGGAAAGTGC CACTCCCCT	480
GTCCCTTCCT AANTAAAAT	499

## (2) INFORMATION FOR SEQ ID NO:74:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

TTTCATAGGA GAACACACTG AGGAGATACT TGAAGAATTT GGATTCAGCC GCGAAGAGAT	60
TTATCAGCTT AACTCAGATA AAATCATTGA AAGTAATAAG GTAAAAGCTA GTCTCTAATC	120
TCCAGGCCCA CGGCTCAAGT GAATTGAAAT ACTGCATTTA CAGTGTAGAG TAACACATAA	180
CATTGTATGC ATGGAAACAT GGAGGAACAG TATTACAGTG TCCTTACACT CTAATCAAGA	240
AAAGAATTAC AGACTCTGAT TCTACAGTGA TGATTGAATT CTAAAAATGG TAATCATTAG	300
GGCTTTGAT TTATAANACT TTGGGTACTT ATACTAAATT ATGGTAGTTA TACTGCCTTC	360
CAGTTGCTT GATATATTG TTGATATTAA GATTCTTGAC TTATATTTG AATGGGTTCT	420
ACTGAAAAAN GAATGATATA TTCTTGAAGA CATCGATATA CATTATTTA CACTCTTGAT	480
TCTACAAATGT AGAAAATGAA GGAAATGCC CAAATTGTAT GGTGATAAAA GTCCCGT	537

## (2) INFORMATION FOR SEQ ID NO:75:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CAAANACAAT TGTTCAAAAG ATGCAAATGA TACACTACTG CTGCAGCTCA CAAACACCTC	60
TGCATATTAC ACGTACCTCC TCCTGCTCCT CAAGTAGTGT GGTCTATTTT GCCATCATCA	120
CCTGCTGTCT GCTTAGAAGA ACGGCTTTCT GCTGCAANG AGAGAAATCA TAACAGACGG	180
TGGCACAAAGG AGGCCATCTT TTCCTCATCG GTTATTGTCC CTAGAAGCGT CTTCTGAGGA	240
TCTAGTTGGG CTTTCTTCTT GGGTTGGGC CATTTCANTT CTCATGTGTG TACTATTCTA	300
TCATTATTGT ATAACGGTTT TCAAACCGNT GGGCACNCAG AGAACCTCAC TCTGTAATAA	360
CAATGAGGAA TAGCCACGGT GATCTCCAGC ACCAAATCTC TCCATGTTNT TCCAGAGCTC	420
CTCCAGCCAA CCCAAATAGC CGCTGCTATN GTGTAGAACA TCCCTGN	467

## (2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

AAGCTGACAG CATTGGGCC GAGATGTCTC GCTCCGTGGC CTTAGCTGTG CTCGCGCTAC	60
TCTCTCTTTC TGGCCTGGAG GCTATCCAGC GTACTCCAAA GATTCAAGGTT TACTCACGTC	120
ATCCAGCAGA GAATGGAAAG TCAAATTTC TGAATTGCTA TGTGTCTGGG TTTCATCCAT	180
CCGACATTGA AGTTGACTTA CTGAAGAATG GAGAGAGAAT TGAAAAAGTG GAGCATTGAG	240
ACTTGTCTTT CAGCAAGGAC TGGTCTTCT ATCTCTTGTA CTACACTGAA TTCACCCCCA	300
CTGAAAAGA TGAGTATGCC TGCGTGTGA ACCATGTGAC TTTGTCACAG CCCAAGATNG	360
TTNAGTGGGA TCGANACATG TAAGCAGCAN CATGGGAGGT	400

## (2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

CTGGAGTGCC TTGGTGTTC AAGCCCCTC AGGAAGCAGA ATGCACCTTC TGAGGCACCT	60
CCAGCTGCC CGGGGGGGG TGCGAGGCTC GGAGCACCCCT TGCCCGGCTG TGATTGCTGC	120
CAGGCACTGT TCATCTCAGC TTTTCTGTCC CTTTGCTCCC GGCAAGCGCT TCTGCTGAA	180
GTTCATATCT GGAGCCTGAT GTCTTAACGA ATAAAGGTCC CATGCTCCAC CCGAAAAAAA	240
AAAAAAAAAA	248

## (2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

ACTAGTCCAG	TGTGGTGGAA	TTCCATTGTG	TTGGGCCAA	CACAATGGCT	ACCTTTAAC	60
TCACCCAGAC	CCCGCCCTGC	CCGTGCCCA	CGCTGCTGCT	AACGACAGTA	TGATGCTTAC	120
TCTGCTACTC	GGAAACTATT	TTTATGTAAT	TAATGTATGC	TTTCTTGT	TTTCTTGT	180
GATTTAAAAA	AAAAAAAAAA	A				201

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

TCCTTTTGTT	AGGTTTTGAGACAACCTA	GACCTAAACT	GTGTCACAGA	CTTCTGAATG	60	
TTTAGGCAGT	GCTAGTAATT	TCCTCGTAAT	GATTCTGTTA	TTACTTTCT	ATTCTTTATT	120
CCTCTTCTT	CTGAAGATTAA	ATGAAGTTGA	AAATTGAGGT	GGATAAAATAC	AAAAAGGTAG	180
TGTGATAGTA	TAAGTATCTA	AGTGCAGATG	AAAGTGTGTT	ATATATATCC	ATTCAAAATT	240
ATGCAAGTTA	GTAATTACTC	AGGGTTAACT	AAATTACTTT	AAATATGCTGT	TGAACCTACT	300
CTGTTCCCTG	GCTAGAAAAA	ATTATAAACAA	GGACTTTGTT	AGTTGGGAA	GCCAAATTGA	360
TAATATTCTA	TGTTCTAAAA	GTTGGGCTAT	ACATAAAANT	TNAAGAAATA	TGGAATTTTA	420
TTCCCAGGAA	TATGGGGTTC	ATTTATGAAT	ANTACCCGGG	ANAGAAGTTT	TGANTNAAAC	480
CNGTTTGGT	TAATACGTTA	ATATGTCCTN	AATNAACAAG	GCNTGACTTA	TTTCCAAAAAA	540
AAAAAAAAAA	AA					552

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

ACAGGGATTT	GAGATGCTAA	GGCCCCAGAG	ATCGTTTGT	CCAACCCCTCT	TATTTTCAGA	60
GGGGAAAATG	GGGCTAGAA	GTTACAGAGC	ATCTAGCTGG	TGCGCTGGCA	CCCCCTGGCCT	120
CACACAGACT	CCCGAGTAGC	TGGGACTTACA	GGCACACAGT	CACTGAAGCA	GGCCCTGTGTT	180
GCAATTACCG	TTGCCACCTC	CAACTTAAAC	ATTCTTCATA	TGTGATGTCC	TTAGTCACTA	240
AGGTTAAACT	TTCCCCACCCA	AAAAAGGCAA	CTTAGATAAA	ATCTTAGAGT	ACTTTCATAC	300

TCTTCTAAAGT CCTCTTCCAG CCTCACTTGT AGTCCTCCTT GGGGGTTGAT AGGAANTNTC	360
TCTTGGCTTT CTCATAAAA TCTCTATCCA TCTCATGTTT AATTTGGTAC GCNTAAAAAT	420
GCTGAAAAAA TTAATGTT CTGGTTTCNC TTTAAAAAAA AAAAAAAA AAAAAAA	476

## (2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

TTTTTTTTTG TATGCCNTCN CTGTGGNGTT ATTGTTGCTG CCACCCTGGA GGAGCCCAGT	60
TTCTTCTGTA TCTTCTTTT CTGGGGGATC TTCTGGCTC TGCCCCTCCA TTCCCAGCCT	120
CTCATCCCCA TCTTGCACTT TTGCTAGGGT TGGAGGCGCT TTCTGGTAG CCCCTCAGAG	180
ACTCAGTCAG CGGAAATAAG TCCTAGGGT GGGGGGTGTG GCAAGCCGGC CT	232

## (2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

AGGCAGGGAGC AGAACGCTAAA GCCAAAGCCC AAGAACAGTG GCAGTGCCAG CACTGGTGCC	60
AGTACCAAGTA CCAATAACAT GCCAGTGCCA GTGCCAGCAC CAGTGGTGGC TTCAGTGCTG	120
GTGCCAGCCT GACGCCACT CTCACATTG GGCTCTTCGC TGGCCTTGGT GGAGCTGGTG	180
CCAGCACCAAG TGGCAGCTCT GGTGCGCTGTG GTTTCCTCCTA CAAGTGAGAT TTTAGATATT	240
GTAAATCCTG CCAGTCTTTC TCTTCAAGCC AGGGTGCATC CTCAGAAACC TACTCAACAC	300
AGCACTCTNG GCAGCCACTA TCAATCAATT GAAGTTGACA CTCTGCATTA AATCTATTTG	360
CCATTTCAAA AAAAAAAA AAA	383

## (2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

ACCGAATTGG GACCGCTGGC TTATAAGCGA TCATGTCTC CAGTATTACC TCAACGAGCA	60
GGGAGATCGA GTCTATAACGC TGAAGAAATT TGACCCGATG GGACAAACAGA CCTGCTCAGC	120
CCATCCTGCT CGGTTCTCCC CAGATGACAA ATACTCTCGA CACCGAATCA CCATCAAGAA	180
ACGCTTCAAG GTGCTCATGA CCCAGCAACC GCGCCCTGTC CTCTGAGGGT CCTTAAACTG	240
ATGTCTTTTC TGCCACCTGT TACCCCTCGG AGACTCCGTA ACCAAACTCT TC GGACTGTG	300
AGCCCCTGATG CCTTTTGCC AGCCATACTC TTTGGCNTCC AGTCTCTCGT GGCGATTGAT	360
TATGCTTGTG TGAGGCAATC ATGGTGGCAT CACCCATNAA GGGAACACAT TTGANTTTT	420
TTTCNCATAT TTTAAATTAC NACCAAGATA NTTCAGAATA AATGAATTGA AAAACTCTTA	480
AAAAAAAAAAA AAAAA	494

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

GCTGGTAGCC TATGGCGTGG CCACGGGANGG GCTCCTGAGG CACGGGACAG TGACTTCCCA	60
AGTATCCTGC GCGCGTCTT CTACCGTCCC TACCTGCAGA TCTTCGGGCA GATTCCCCAG	120
GAGGACATGG ACGTGGCCCT CATGGAGCAC AGCAACTGCT CGTCGGAGCC CGGCTTCTGG	180
GCACACCCCTC CTGGGGCCCA GGCGGGCACCC TGCGTCTCCC AGTATGCCA CTGGCTGGTG	240
GTGCTGCTCC TCGTCATCTT CCTGCTCGTG GCCAACATCC TGCTGGTCAC TTGCTCATTG	300
CCATGTTCAAG TTACACATTC GGCAAAGTAC AGGGCAACAG CNATCTCTAC TGGGAAGGCC	360
AGCGTTNCCG CCTCATCCGG	380

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GAGTTAGCTC CTCCACAACC TTGATGAGGT CGTCTGCAGT GGCCTCTCGC TTCATACCGC	60
TNCCATCGTC ATACTGAGG TTTGCCACCA CCTCCTGCAT CTTGGGGCGG CTAATATCCA	120
GGAAACTCTC AATCAAGTCA CCGTCNATNA AACCTGTGGC TGGTTCTGTC TTCCGCTCGG	180
TGTGAAAGGA TCTCCAGAAG GAGTGCTCGA TCTTCCCCAC ACTTTTGATG ACTTTATTGA	240
GTCGATTCTG CATGCCAGC AGGAGGTTGT ACCAGCTCTC TGACAGTGAG GTCACCAGCC	300
CTATCATGCC NTTGAAACGTG CCGAAGAACCA CCGAGCCTTG TGTGGGGGGT GNAGTCTCAC	360
CCAGATTCTG CATTACCAAGA NAGCCGTGGC AAAAGANATT GACAACCTCGC CCAGGNNNGAA	420
AAAGAACACC TCCTGGAAGT GCTNGCCGCT CCTCGTCCNT TGGTGGNNNGC GCNTNCCTTT	480
T	481

## (2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

AACATCTTCC TGTATAATGC TGTGTAATAT CGATCCGATN TTGTCTGCTG AGAATTCA	60
ACTTGGAAAA GCAACTTNAA GCCTGGACAC TGGTATTAAA ATTACAATA TGCAACACTT	120
TAAACAGTGT GTCAATCTGC TCCCTTACTT TGTCATCACC AGTCTGGAA TAAGGGTATG	180
CCCTATTCAACCTGTTAAA AGGGCGCTAA GCATTTTGAA TTCAACATCT TTTTTTTGAA	240
CACAAGTCCG AAAAAGCAA AAGTAAACAG TTNTTAATTGTTAGCCAAT TCACCTTC	300
CATGGGACAG AGCCATTGAA TTAAAAAAGC AAATTGCATA ATATTGAGCT TTGGGAGCTG	360
ATATNTGAGC GGAAGANTAG CCTTTCTACT TCACCAAGACA CAACTCCCTT CATATTGGGA	420
TGTTNACNAAGTATGTCT CTTACAGATG GGATGCTTT GTGGCAATTCTG	472

## (2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 413 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

AGAAACCACT ATCTCTNAAC ACAACCTCTC ATACCTTGAG GACCTAATTG TGTGTGCGTG	60
TGTGTGCGCG CGCATATTAT ATAGACAGGC ACATCTTTT TACTTTGTA AAAGCTTATG	120
CCTCTTGGT ATCTATATCT GTGAAAGTTT TAATGATCTG CCATAATGTC TTGGGGACCT	180
TGTGCTTCTG TGAAATGGT ACTAGAGAAA ACACCTATNT TATGAGTCAA TCTAGTTNGT	240
TTTATTGAC ATGAAGGAAA TTCCAGATN ACAACACTNA CAAACTCTCC CTTGACTAGG	300
GGGGACAAAG AAAAGCANAAG CTGAACATNA GAAACAATTN CCTGGTGAGA AATTNCATAA	360

ACAGAAATTG GGTNGTATAT TGAAANANNG CATCATTNAA ACGTTTTTT TTT

413

## (2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CGCAGCGGGT CCTCTCTATC TAGCTCCAGC CTCTCGCCTG	CCCCACTCCC CGCGTCCCGC	60
GTCCTAGCCN ACCATGCCG GGCCCTGCG CGCCCGCTG	CTCCCTGCTGG CCATCCTGGC	120
CGTGGCCCTG GCCGTGAGCC CCGCGGCCGG CTCCAGTCCC	GGCAAGCCGC CGCGCCTGGT	180
GGGAGGCCA TGGACCCCGC GTGGAAGAAG AAGGTGTGCG	CCGTGCCTG GACTTTGCCG	240
TCGGCNANTA CAACAAACCC GCAACNACTT TTACCNAGCN	CGCGCTGCAG GTTGTGCCGC	300
CCCAANCAAA TTGTTACTNG GGGTAANTAA TTCTTGAAG	TTGAACCTGG GCCAAACNN	360
TTTACCAAGAA CCNAGCCAAT TNGAACAATT NCCCTCCAT	AACAGCCCT TTTAAAAAGG	420
GAANCANTCC TGNCTTTTC CAAATT		448

## (2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GAATTGTG CACTGGCAC TGTGATGAA CCATTGGCC AGGATGCTT GAGTTATCA	60
GTAGTGATTC TGCAAAGTT GGTGTTGAA CATGAGTATG TAAAATGTCA AAAAATTAGC	120
AGAGGTCTAG GTCTGCATAT CAGCAGACAG TTTGTCCGTG TATTTGTAG CCTTGAAGTT	180
CTCAGTGACA AGTTNNTCT GATGCGAAGT TCTNATTCCA GTGTTTAGT CCTTGACATC	240
TTTNATGTT AGACTTGCT CTNTAAATT GCTTTGTNT TCTGCAGGTA CTATCTGTGG	300
TTAACAAAA TAGAANNACT TCTCTGCTT GAANATTG AATATCTTACA TCTNAAAATN	360
AATTCTCTCC CCATANAAA ACCCANGCCC TTGGGANAAT TTGAAAANG GNTCCTTCNN	420
AATTCCNNANA ANTTCAGNTN TCATACAACA NAACNGGANC CCC	463

## (2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

AGGGATTGAA GGTCTNTTNT ACTGTCGGAC TGTTCANCCA CCAACTCTAC AAGTTGCTGT	60
CTTCCACTCA CTGTCGTAA GCNTNTTAAC CCAGACTGTA TCTTCATAAA TAGAACAAAT	120
TCTTCACCAG TCACATCTTC TAGGACCTTT TTGGATTCAAG TTAGTATAAG CTCTTCCACT	180
TCCTTTGTTA AGACTTCATC TGGTAAAGTC TTAAGTTTG TAGAAAGGAA TTTAATTGCT	240
CGTTCTCTAA CAATGTCCTC TCCTTGAAGT ATTTGGCTGA ACAACCCACC TNAAGTCCCT	300
TTGTGCATCC ATTTTAAATA TACTTAATAG GGCATTGGTN CACTAGGTTA AATTCTGCAA	360
GAGTCATCTG TCTGCAAAAG TTGCGTTAGT ATATCTGCCA	400

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 480 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GAGCTCGGAT CCAATAATCT TTGTCTGAGG GCAGCACACA TATNCAGTGC CATGGNAACT	60
GGTCTACCCC ACATGGGAGC AGCATGCCGT AGNTATATAA GGTCAATTCCC TGAGTCAGAC	120
ATGCTCTTT GACTACCGTG TGCCAGTGC GGTGATTCTC ACACACCTCC NNCCGCTCTT	180
TGTGGAAAAA CTGGCACTTG NCTGGAACTA GCAAGACATC ACTTACAAAT TCACCCACGA	240
GACACTTGAA AGGTGTAACA AAGCGACTCT TGCATTGCTT TTTGTCCCTC CGGCACCAAGT	300
TGTCAATACT AACCCGCTGG TTGCTCTCCA TCACATTGT GATCTGTAGC TCTGGATACA	360
TCTCCTGACA GTACTGAAGA ACTTCTTCTT TTGTTTCAAA AGCAACTCTT GGTGCCTGTT	420
NGATCAGGTT CCCATTCCC AGTCCGAATG TTCACATGGC ATATNTTACT TCCCACAAAAA	480

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 477 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

ATACAGCCCCA	NATCCCACCA	CGAAGATGCG	CTTGTGACT	GAGAACCTGA	TGCGGTCACT	60
GGTCCCGCTG	TAGCCCCAGC	GACTCTCCAC	CTGCTGGAAG	CGGTTGATGC	TGCACTCCTT	120
CCCACGCAGG	CAGCAGCGGG	GCCGGTCAAT	GAACTCCACT	CGTGGCTTGG	GGTTGACGGT	180
TAANTGCAGG	AAGAGGCTGA	CCACCTCGCG	GTCCACCAGG	ATGCCCGACT	GTGCGGGACC	240
TGCAGCGAAA	CTCCTCGATG	GTCATGAGCG	GGAAAGCGAAT	GANGCCCAGG	GCCTTGCCCA	300
GAACCTTCCG	CCTGTTCTCT	GGCGTCACCT	GCAGCTGCTG	CCGCTNACAC	TCGGCCTCGG	360
ACCAGCGGAC	AAACGGCGTT	GAACAGCCGC	ACCTCACCGA	TGCCCANTGT	GTCGCGCTCC	420
AGGAACGGCN	CCAGCGTGTG	CAGGTCAATG	TCGGTGAANC	CTCCGCGGGT	AATGGCG	477

## (2) INFORMATION FOR SEQ ID NO:93:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GAACGGCTGG	ACCTTGCCTC	GCATTGTGCT	GCTGGCAGGA	ATACCTTGGC	AAGCAGCTCC	60
AGTCCGAGCA	GCCCCAGACC	GCTGCCGCC	GAAGCTAACG	CTGCCTCTGG	CCTTCCCCTC	120
CGCCTCAATG	CAGAACCAANT	AGTGGGAGCA	CTGTGTTAG	AGTTAAGAGT	GAACACTGTN	180
TGATTTTACT	TGGGAATTC	CTCTGTTATA	TAGCTTTTCC	CAATGCTAAT	TTCCAAACAA	240
CAACAACAAA	ATAACATGTT	TGCCGTGTTNA	GTTGTATAAA	AGTANGTGAT	TCTGTATNTA	300
AAGAAAATAT	TACTGTTACA	TATACTGCTT	GCAANTTCTG	TATTATTGG	TNCTCTGGAA	360
ATAAAATATAT	TATTAAA					377

## (2) INFORMATION FOR SEQ ID NO:94:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CCCTTTGAGG	GGTTAGGGTC	CAGTTCCAG	TGGAAGAAC	AGGCCAGGAG	AANTGCGTGC	60
CGAGCTGANG	CAGATTTCCC	ACAGTGACCC	CAGAGCCCTG	GGCTATAGTC	TCTGACCCCT	120
CCAAGGAAAG	ACCACCTCT	GGGGACATGG	GCTGGAGGGC	AGGACCTAGA	GGCACCAAGG	180
GAAGGCCCA	TTCCGGGCT	GTTCCCCGAG	GAGGAAGGGA	AGGGGCTCTG	TGTGCCCTCC	240
ACGAGGAANA	GGCCCTGANT	CCTGGGATCA	NACACCCCTT	CACGTGTATC	CCCACACAAA	300

TGCAAGCTCA CCAAGGTCCC CTCTCAGTCC CTTCCCTACA CCCTGAACGG NCACTGGCCC  
 ACACCCACCC AGANCANCCA CCCGCCATGG GGAATGTNCT CAAGGAATCG CNGGGCAACG  
 TGGACTCTNG TCCCNNAAAGG GGGCAGAATC TCCAATAGAN GGANNGAAC CTTGCTNANA  
 AAAAAAAANA AAAAAA 360  
 420  
 480  
 495

## (2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 472 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GGTTACTTGG TTTCATTGCC ACCACTTAGT GGATGTCATT TAGAACCATT TTGTCCTGCTC  
 CCTCTGGAAG CCTTGCAG AGCGGACTTT GTAATTGTTG GAGAATAACT GCTGAATTTT  
 TAGCTGTTT GAGTTGATT GCACCACTGC ACCACAACCTC AATATGAAAAA CTATTTNACT  
 TATTTATTAT CTTGTGAAAAA GTATACAATG AAAATTGTTG TCATACTGTA TTTATCAAGT  
 ATGATGAAAAA GCAATAGATA TATATTCTTT TATTATGTTN AATTATGATT GCCATTATTA  
 ATCGGCAAAA TGTGGAGTGT ATGTTCTTTT CACAGTAATA TATGCCTTTT GTAACTTCAC  
 TTGGTTATTT TATTGTAAAT GAATTACAAA ATTCTTAATT TAAGAAAATG GTANGTTATA  
 TTTANTTCAN TAATTCTTT CCTTGTAC GTTAATTG AAAAGAATGC AT 60  
 120  
 180  
 240  
 300  
 360  
 420  
 472

## (2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 476 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

CTGAAGCATT TCTTCAAAC TNTCTACTTT TGTCATTGAT ACCTGTAGTA AGTTGACAAT 60  
 GTGGTGAAT TTCAAAATTA TATGTAACCTT CTACTAGTTT TACTTTCTCC CCCAAGTCTT  
 TTTTAACCTCA TGATTTTAC ACACACAATC CAGAACTTAT TATATAGCCT CTAAGTCTTT  
 ATTCTTCACA GTAGATGATG AAAGAGTCCT CCAGTGTCTT GNCGANAATG TTCTAGNTAT 120  
 AGCTGGATAC ATACNGTGGG AGTTCTATAA ACTCATACTT CAGTGGACT NAACCAAAAT  
 TGTGTTAGTC TCAATTCTCA CCACACTGAG GAGCCTCCC AAATCACTAT ATTCTTATCT 180  
 GCAGGTTACTC CTCCAGAAAA ACNGACAGGG CAGGCTTGCA TGAAAAAGTN ACATCTGCGT  
 TACAAAGTCT ATCTTCCTCA NANGTCTGTN AAGGAACAAT TTAATCTTCT AGCTTT 240  
 300  
 360  
 420  
 476

## (2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 479 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

ACTCTTTCTA ATGCTGATAT GATCTTGAGT ATAAGAATGC ATATGTCACT AGAATGGATA	60
AAATAATGCT GCAAACCTAA TGTCTTATG CAAAATGGAA CGCTAATGAA ACACAGCTTA	120
CAATCGAAA TCAAAACTCA CAAGTGTCA TCTGTTGTAG ATTTAGTGTAA ATAAGACTTA	180
GATTGTGCTC CTTCGGATAT GATTGTTCT CANATCTTGG GCAATNTTCC TTAGTCAAAT	240
CAGGCTACTA GAATTCTGTT ATTGGATATN TGAGAGCATG AAATTTTAA NAATACACTT	300
GTGATTATNA AATTAATCAC AAATTCACT TATACCTGCT ATCAGCAGCT AGAAAAACAT	360
NTNNNTTTTA NATCAAAGTA TTTTGTGTTT GGAANTGTNN AAATGAAATC TGAATGTGGG	420
TTCNATCTTA TTTTTTCCCN GACNACTANT TNCTTTTTA GGGNCTATTG TGANCCATC	479

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 461 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

AGTGACTTGT CCTCCAACAA AACCCCTTGA TCAAGTTGT GGCACTGACA ATCAGACCTA	60
TGCTAGTTCC TGTCTATCTAT TCGCTACTAA ATGCAGACTG GAGGGGACCA AAAAGGGGCA	120
TCAACTCCAG CTGGATTATT TTGGAGCCTG CAAATCTATT CCTACTTGTA CGGACTTTGA	180
AGTGATTCAAG TTTCCCTCTAC GGATGAGAGA CTGGCTCAAG AATATCCTCA TGCACTTTA	240
TGAAGCCACT CTGAACACGC TGTTATCTA GATGAGAACAA GAGAAATAAA GTCAGAAAAT	300
TTACCTGGAG AAAAGAGGCT TTGGCTGGGG ACCATCCCCT TGAAACCTTCT CTTAAGGACT	360
TTAAGAAAAA CTACCACATG TTGTGTATCC TGGTGCCTGC CGTTTATGAA CTGACCACCC	420
TTTGAATAA TCTTGACGCT CCTGAACCTTG CTCCTCTGCG A	461

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 171 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GTGGCCGCGC GCAGGTGTTT CCTCGTACCG CAGGGCCCCC TCCCTTCCCC AGGCCTCCCT	60
CGGCGCCTCT GCAGGGCCGA GGAGGAGCGG CTGGCGGGTG GGGGGAGTGT GACCCACCCCT	120
CGGTGAGAAA AGCCTTCTCT AGCGATCTGA GAGGCGTGCC TTGGGGGTAC C	171

## (2) INFORMATION FOR SEQ ID NO:100:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

CGGCCGCAAG TGCAACTCCA GCTGGGGCCG TGCGGACGAA GATTCTGCCA GCAGTTGGTC	60
CGACTGCGAC GACGGCGCG GCGACAGTCG CAGGTGCAGC GCGGGCGCCT GGGGTCTTGC	120
AAGGCTGAGC TGACGCCGCA GAGGTCGTGT CACGTCCCAC GACCTTGACG CCGTCGGGGA	180
CAGCCGGAAC AGAGCCCGGT GAAGCGGGAG GCCTCGGGGA GCCCCTCGGG AAGGGCGGCC	240
CGAGAGATAAC GCAGGTGCAG GTGGCCGCC	269

## (2) INFORMATION FOR SEQ ID NO:101:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TTTTTTTTTT TTTTGGAAATC TACTGCGAGC ACAGCAGGTC AGCAACAAAGT TTATTTGCA	60
GCTAGCAAGG TAACAGGGTA GGGCATGGTT ACATGTTCAAG GTCAACTTCC TTTGTCGTGG	120
TTGATTGGTT TGTCTTATG GGGGCGGGGT GGGGTAGGGG AAACGAAGCA AATAACATGG	180
AGTGGGTGCA CCCTCCCTGT AGAACCTGGT TACAAAGCTT GGGCAGTTC ACCTGGTCTG	240
TGACCGTCAT TTTCTTGACA TCAATGTTAT TAGAAGTCAG GATATCTTT AGAGAGTCCA	300
CTGTTCTGGA GGGAGATTAG GTTTCTTGC CAAATCCAAC AAAATCCACT GAAAAAGTTG	360
GATGATCAGT ACGAATACCG AGGCATATTC TCATATCGGT GGCCCA	405

## (2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 470 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT	60
GGCACTTAAT CCATTTTAT TTCAAAATGT CTACAAATTT AATCCCATT ACGGTATTT	120
TCAAAATCTA AATTATTCAA ATTAGCCAA TCCTTACCAA ATAATACCCA AAAATCAAAA	180
ATATACTTCT TTCAGCAAAC TTGTTACATA AATTAAAAAA ATATATAACGG CTGGTGTTT	240
CAAAGTACAA TTATCTAAC ACTGCAAACA TTTTAAGGAA CTAAAATAAA AAAAAACACT	300
CCGCAAAGGT TAAAGGGAAC AACAAATTCT TTTACAACAC CATTATAAAA ATCATATCTC	360
AAATCTTAGG GGAATATATA CTTCACACGG GATCTTAAC TTTACTCACT TTGTTTATTT	420
TTTTAAACCA TTGTTGGC CCAACACAAT GGAATCCCCC CTGGACTAGT	470

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 581 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

TTTTTTTTTT TTTTTTTTGA CCCCCCTCTT ATAAAAAAC A GTTACCAT T TATTTTACT	60
TACACATATT TATTTTATAA TTGGTATTAG ATATTCAAAA GGCAGCTTT AAAATCAAAC	120
TAAATGGAAA CTGCCTTAGA TACATAATTC TTAGGAATTA GCTTAAATC TGCCTAAAGT	180
GAAAATCTC TCTAGCTCTT TTGACTGTAA ATTTTGACT CTTGTAAAAC ATCCAAATTC	240
ATTTTCTTG TCTTTAAAT TATCTAATCT TTCCATT TTTT CCCCTATTCC AAGTCATTT	300
GCTTCTCTAG CCTCATTCC TAGCTTTAT CTACTATTAG TAAGTGGCTT TTTTCTAAA	360
AGGGAAAACA GGAAGAGAAA TGGCACACAA AACAAACATT TTATATTCA T ATTTCTACCT	420
ACGTTAATAA AATAGCATTT TGTGAAGCCA GCTAAAAGA AGGCTTAGAT CCTTTTATGT	480
CCATTTAGT CACTAACGA TATCAAAGTG CCAGAATGCA AAAGGTTGT GAACATTAT	540
TCAAAAGCTA ATATAAGATA TTTCACATAC TCATCTTCT G	581

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 578 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

TTTTTTTTTT	TTTTTTTTTT	TTTTTCTCTT	CTTTTTTTTT	GAAATGAGGA	TCGAGTTTTT	60
CACTCTCTAG	ATAGGGCATG	AAGAAAACTC	ATCTTCCAG	CTTAAATAA	ACAATCAAAT	120
CTCTTATGCT	ATATCATATT	TTAAGTTAAA	CTAATGAGTC	ACTGGCTTAT	CTTCTCCTGA	180
AGGAAATCTG	TTCATTCTTC	TCATTCAAT	AGTTATATCA	AGTACTACCT	TGCATATTGA	240
GAGGTTTTTC	TTCTCTATTT	ACACATATAT	TTCCATGTGA	ATTGTATCA	AACCTTTATT	300
TTCATGAAA	CTAGAAAATA	ATGTTTCTTT	TGCATAAGAG	AAGAGAACAA	TATAGCATTA	360
CAAAACTGCT	CAAATTGTTT	GTAAAGTTAT	CCATTATAAT	TAGTTGGCAG	GAGCTAATAC	420
AAATCACATT	TACGACAGCA	ATAATAAAAC	TGAAGTACCA	GTAAATATC	CAAATAATT	480
AAAGGAACAT	TTTAGCCTG	GGTATAATTA	GCTAATTAC	TTTACAAGCA	TTTATTAGAA	540
TGAATTACCA	TGTTATTATT	CCTAGCCAA	CACAATGG			578

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 538 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

TTTTTTTTTT	TTTTTCAGTA	ATAATCAGAA	CAATATTAT	TTTTATATTT	AAAATTCTATA	60
GAAAAGTGCC	TTACATTTAA	AAAAGTTTG	TTCTCTAAAG	TGATCAGAGG	AATTAGATAT	120
GTCTTGAACA	CCAATATTAA	TTGAGGAAA	ATACACCAAA	ATACATTAAG	TAAATTATTT	180
AAGATCATAG	AGCTTGTAAG	TGAAAAGATA	AAATTGACC	TCAGAAACTC	TGAGCATTAA	240
AAATCCACTA	TTAGCAAATA	AATTACTATG	GACTTCTTGC	TTAATTTCG	TGATGAATAT	300
GGGGTGTAC	TGGTAAACCA	ACACATTCTG	AAGGATACAT	TACTTAGTGA	TAGATTCTTA	360
TGTACTTTGC	TAATACGTGG	ATATGAGTTG	ACAAGTTCT	CTTCTTCAA	TCTTTAAGG	420
GGCGAGAAAT	GAGGAAGAAA	AGAAAAGGAT	TACGCATACT	GTTCTTCTA	TGGAAGGATT	480
AGATATGTTT	CCTTGCCAA	TATTAACAAA	ATAATAATGT	TTACTACTAG	TGAAACCC	538

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

TTTTTTTTTT TTTTTAGTC AAGTTTCTAT TTTTATTATA ATTAAAGTCT TGGTCATTTC	60
ATTTATTAGC TCTGCAACTT ACATATTAA ATTAAAGAAA CGTTTAGAC AACTGTACAA	120
TTTATAAATG TAAGGTGCCA TTATTGAGTA ATATATTCCCT CCAAGAGTGG ATGTGTCCCT	180
TCTCCCAACCA ACTAATGAAC AGCAACATTA GTTTAATTTT ATTAGTAGAT ATACACTGCT	240
GCAAACGCTA ATTCTCTTCT CCATCCCCAT GTGATATTGT GTATATGTGT GAGTTGGTAG	300
AATGCATCAC AATCTACAAT CAACAGCAAG ATGAAGCTAG GCTGGGCTTT CGGTGAAAAT	360
AGACTGTGTC TGTCTGAATC AAATGATCTG ACCTATCCTC GGTGGCAAGA ACTCTTCGAA	420
CCGCTTCCTC AAAGGCCTG CCACATTGT GGCTCTTGC ACTTGTTC AAA	473

## (2) INFORMATION FOR SEQ ID NO:107:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CGCCATGGCA CTGCAGGGCA TCTCGGTCA GGAGCTGTCC GGCTGGCCC CGGGCCCGTT	60
CTGTGCTATG GTCCTGGCTG ACTTCGGGGC GCGTGTGGTA CGCGTGGACC GGCCCCGGCTC	120
CCGCTACGAC GTGAGCCGCT TGGGCCGGGG CAAGCGCTCG CTAGTGCTGG ACCTGAAGCA	180
GCCGCGGGGA GCCGCCGTGC TCGGGCGTCT GTGCAAGCGG TCGGATGTGC TGCTGGAGCC	240
CTTCCGCCGC GGTGTATGG AGAAACTCCA GCTGGGCCA GAGATTCTGC AGCGGGAAAA	300
TCCAAGGCTT ATTTATGCCA GGCTGAGTGG ATTTGGCCAG TCAGGAAGCT TCTGCCGGTT	360
AGCTGGCCAC GATATCAACT ATTTGGCTTT GTCAGGTGTT CTCTCAAAAA TTGGCAGAAG	420
TGGTGAGAAT CCGTATGCC CGCTGAATCT CCTGGCTGAC TTTGCTGGTG GTGGCCTTAT	480
GTGTGCACTG GCCATTATAA TGGCTCTTT TGACCGCACA CGCACTGACA AGGGTCAGGT	540
CATTGATGCA AATATGGTGG AAGGAACAGC ATATTTAAGT TCTTTCTGT GGAAAACCTCA	600
GAAATCGAGT CTGTGGGAAG CACCTCGAGG ACAGAACATG TTGGATGGTG GAGCACCTTT	660
CTATACGACT TACAGGACAG CAGATGGGG ATTCACTGGCT GTTGGAGCAA TAGAACCCCA	720
GTCTACGAG CTGCTGATCA AAGGACTTGG ACTAAAGTCT GATGAACCTTC CCAATCAGAT	780
GAGCATGGAT GATTGGCCAG AAATGAAGAA GAAGTTTGCA GATGTATTTG CAAAGAACAC	840
GAAGGCAGAG TGGTGTCAAA TCTTGACGG CACAGATGCC TGTGTGACTC CGGTTCTGAC	900
TTTGAGGAG GTTGTTCATC ATGATCACAA CAAGGAACGG GGCTCGTTA TCACCACTGA	960
GGAGCAGGAC GTGAGCCCCC GCCCTGCACC TCTGCTGTTA AACACCCCA CGATCCCTTC	1020
TTTCAAAAGG GATCCTTCA TAGGAGAACAA CACTGAGGAG ATACTTGAAAG AATTGGATT	1080
CAGCCCGAA GAGATTTCATC AGCTTAACTC AGATAAAATC ATTGAAAGTA ATAAGGTAAA	1140
AGCTAGTCTC TAACTCCAG GCCCACGGCT CAAGTGAATT TGAATACTGC ATTTACAGTG	1200
TAGAGTAACA CATAACATTG TATGCATGGA AACATGGAGG AACAGTATTA CAGTGTCTA	1260
CCACTCTAAT CAAGAAAAGA ATTACAGACT CTGATTCTAC AGTGATGATT GAATTCTAA	1320
AATGGTTATC ATTAGGGCTT TTGATTATAA AAACTTGGG TACTTATACT AAATTATGGT	1380
AGTTATTCTG CCTTCCAGTT TGCTTGATAT ATTTGTTGAT ATTAAGATTC TTGACTTATA	1440
TTTGAAATGG GTTCTAGTGA AAAAGGAATG ATATATTCTT GAAGACATCG ATATACATTT	1500
ATTTACACTC TTGATTCTAC AATGTAGAAA ATGAGGAAAT GCCACAAATT GTATGGTAG	1560

AAAAGTCACG TGAAACAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA  
 A 1620  
 1621

## (2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 382 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

Met Ala Leu Gln Gly Ile Ser Val Met Glu Leu Ser Gly Leu Ala Pro  
 1 5 10 15  
 Gly Pro Phe Cys Ala Met Val Leu Ala Asp Phe Gly Ala Arg Val Val  
 20 25 30  
 Arg Val Asp Arg Pro Gly Ser Arg Tyr Asp Val Ser Arg Leu Gly Arg  
 35 40 45  
 Gly Lys Arg Ser Leu Val Leu Asp Leu Lys Gln Pro Arg Gly Ala Ala  
 50 55 60  
 Val Leu Arg Arg Leu Cys Lys Arg Ser Asp Val Leu Leu Glu Pro Phe  
 65 70 75 80  
 Arg Arg Gly Val Met Glu Lys Leu Gln Leu Gly Pro Glu Ile Leu Gln  
 85 90 95  
 Arg Glu Asn Pro Arg Leu Ile Tyr Ala Arg Leu Ser Gly Phe Gly Gln  
 100 105 110  
 Ser Gly Ser Phe Cys Arg Leu Ala Gly His Asp Ile Asn Tyr Leu Ala  
 115 120 125  
 Leu Ser Gly Val Leu Ser Lys Ile Gly Arg Ser Gly Glu Asn Pro Tyr  
 130 135 140  
 Ala Pro Leu Asn Leu Leu Ala Asp Phe Ala Gly Gly Leu Met Cys  
 145 150 155 160  
 Ala Leu Gly Ile Ile Met Ala Leu Phe Asp Arg Thr Arg Thr Asp Lys  
 165 170 175  
 Gly Gln Val Ile Asp Ala Asn Met Val Glu Gly Thr Ala Tyr Leu Ser  
 180 185 190  
 Ser Phe Leu Trp Lys Thr Gln Lys Ser Ser Leu Trp Glu Ala Pro Arg  
 195 200 205  
 Gly Gln Asn Met Leu Asp Gly Gly Ala Pro Phe Tyr Thr Thr Tyr Arg  
 210 215 220  
 Thr Ala Asp Gly Glu Phe Met Ala Val Gly Ala Ile Glu Pro Gln Phe  
 225 230 235 240  
 Tyr Glu Leu Leu Ile Lys Gly Leu Gly Leu Lys Ser Asp Glu Leu Pro  
 245 250 255  
 Asn Gln Met Ser Met Asp Asp Trp Pro Glu Met Lys Lys Lys Phe Ala  
 260 265 270  
 Asp Val Phe Ala Lys Lys Thr Lys Ala Glu Trp Cys Gln Ile Phe Asp  
 275 280 285  
 Gly Thr Asp Ala Cys Val Thr Pro Val Leu Thr Phe Glu Glu Val Val

290	295	300
His His Asp His Asn Lys	Glu Arg Gly Ser Phe Ile Thr Ser Glu Glu	
305	310	315
Gln Asp Val Ser Pro Arg Pro Ala Pro	Leu Leu Leu Asn Thr Pro Ala	320
325	330	335
Ile Pro Ser Phe Lys Arg Asp Pro	Phe Ile Gly Glu His Thr Glu Glu	
340	345	350
Ile Leu Glu Glu Phe Gly Phe Ser Arg	Glu Glu Ile Tyr Gln Leu Asn	
355	360	365
Ser Asp Lys Ile Ile Glu Ser Asn Lys	Val Lys Ala Ser Leu	
370	375	380

## (2) INFORMATION FOR SEQ ID NO:109:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1524 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GGCACGAGGC	TGCGCCAGGG	CCTGAGCGGA	GGCGGGGGCA	GCCTCGCCAG	CGGGGGCCCC	60
GGCCCTGGCC	ATGCCTCACT	GAGCCAGCGC	CTGCGCTCT	ACCTCGCCGA	CAGCTGAAAC	120
CAGTGCAGCC	TAGTGGCTCT	CACCTGCTTC	CTCCTGGCG	TGGGCTGCCG	GCTGACCCCG	180
GGTTTGTACC	ACCTGGGCCG	CACTGTCTC	TGCATCGACT	TCATGGTTTT	CACGGTGCAG	240
CTGCTTCACA	TCTTCACGGT	CAACAAACAG	CTGGGGCCCA	AGATCGTCAT	CGTGAGCAAG	300
ATGATGAAGG	ACGTGTTCTT	CTTCCTCTTC	TTCCCTGGCG	TGTGGCTGGT	AGCCTATGGC	360
GTGCCACCGG	AGGGGCTCCT	GAGGCCACGG	GACAGTGACT	TCCCAAGTAT	CCTGCGCCGC	420
GTCTTCTACC	GTCCCTACCT	GCAGATCTTC	GGGCAGATTG	CCCAGGAGGA	CATGGACGTG	480
GCCCTCATGG	AGCACAGCAA	CTGCTCGTCG	GAGCCCGGCT	TCTGGGCACA	CCCTCCTGGG	540
GCCAGGCGG	GCACCTGCGT	CTCCCAGTAT	GCCAAGTGGC	TGGTGGTGC	GCTCCTCGTC	600
ATCTTCCTGC	TCGTGGCCAA	CATCCTGCTG	GTCAACTTGC	TCATTGCCAT	GTTCAGTTAC	660
ACATTGGCA	AAGTACAGGG	QAACAGCGAT	CTCTACTTGG	AGGCGCAGCG	TTACCGCCTC	720
ATCCGGGAAT	TCCACTCTCG	GCCCCGGCTG	GCCCCGGCCCT	TTATCGTCAT	CTCCCACCTG	780
CGCCTCCTGC	TCAGGCAATT	GTGCAGGGCA	CCCCGGAGCC	CCCAGCGTC	CTCCCCGGCC	840
CTCGAGCATT	TCCGGGTTTA	CCTTTCTAAG	GAAGCCGAGC	GGAAGCTGCT	AACGTGGAA	900
TCGGTGCATA	AGGAGAACCT	TCTGCTGGCA	CGCGCTAGGG	ACAAGCGGGA	GAGCGACTCC	960
GAGCGTCTGA	AGCGCACGTC	CCAGAACGGT	GACTTGGCAC	TGAAACAGCT	GGGACACATC	1020
CGCGAGTACG	AACAGCGCCT	GAAAGTGCTG	GAGCGGGAGG	TCCAGCAGTG	TAGCCCGGTC	1080
CTGGGGTGGG	TGGCCGAGGC	CCTGAGCCGC	TCTGCCTTGC	TGCCCCCAGG	TGGGCGGCCA	1140
CCCCCTGACC	TGCCTGGTC	CAAAGACTGA	GCCCCTGCTGG	CGGACTTCAA	GGAGAACGCC	1200
CCACAGGGGA	TTTTGCTCCT	AGAGTAAGGC	TCATCTGGGC	CTCGGCCCCC	GCACCTGGTG	1260
GCCTTGTCTT	TGAGGTGAGC	CCCATGTCCA	TCTGGGCCAC	TGTCAGGACC	ACCTTTGGGA	1320
GTGTCACTCT	TACAAACCAC	AGCATGCCG	GCTCCTCCCA	GAACCAGTCC	CAGCCTGGGA	1380
GGATCAAGGC	CTGGATCCCG	GGCCGTTATC	CATCTGGAGG	CTGCAGGGTC	CTTGGGGTAA	1440
CAGGGACCAC	AGACCCCTCA	CCACTCACAG	ATTCCCTCACA	CTGGGGAAAT	AAAGCCATT	1500
CAGAGGAAAA	AAAAAAAAAA	AAAA				1524

## (2) INFORMATION FOR SEQ ID NO:110:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3410 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GGGAACCAGC	CTGCACCGCGC	TGGCTCCGGG	TGACAGCCGC	GCGCCTCGGC	CAGGATCTGA	60
GTGATGAGAC	GTGTCACCAC	TGAGGTGCC	CACAGCAGCA	GGTGGTGGAGC	ATGGGCTGAG	120
AAGCTGGACC	GGCACCAAAG	GGCTGGCAGA	AATGGGCGCC	TGGCTGATT	CTAGGCAGTT	180
GGCGGCAGCA	AGGAGGAGAG	GCCGCAGCTT	CTGGAGCAGA	GCCGAGACGA	AGCAGTTCTG	240
GAGTGCCTGA	ACGGCCCCCT	GAGCCCTACC	CGCCTGGCCC	ACTATGGTCC	AGAGGCTGTG	300
GGTGGAGCCGC	CTGCTGCGGC	ACCGGAAAGC	CCAGCTCTTG	CTGGTCAACC	TGCTAACCTT	360
TGGCCTGGAG	GTGTGTTTGG	CCGCAGGCAT	CACCTATGTG	CCGCCTCTGC	TGCTGGAAGT	420
GGGGGTAGAG	GAGAAGTTCA	TGACCATGGT	GCTGGGCATT	GGTCCAGTGC	TGGGCTGGT	480
CTGTGTCCCC	CTCCTAGGCT	CAGCCAGTGA	CCACTGGCGT	GGACGCTATG	GCCGCCGCCG	540
GCCCTTCATC	TGGGCACTGT	CCTTGGGCAT	CCTGCTGAGC	CTCTTTCTCA	TCCCAAGGGC	600
CGGCTGGCTA	GCAGGGCTGC	TGTGCCCCGA	TCCCAGGCC	CTGGAGCTGG	CACTGCTCAT	660
CCTGGGGCTG	GGGCTGCTGG	ACTTCTGTGG	CCAGGTGTGC	TTCACTCCAC	TGGAGGCCCT	720
GCTCTCTGAC	CTCTTCCGGG	ACCCGGACCA	CTGTCGCCAG	GCTTACTCTG	TCTATGCCCT	780
CATGATCAGT	CTTGGGGCT	GCCTGGGCTA	CCTCCTGCCT	GCCATTGACT	GGGACACCA	840
TGCCCTGGCC	CCCTACCTGG	GCACCCAGGA	GGAGTGCCTC	TTTGGCCTGC	TCACCCCTCAT	900
CTTCCTCACC	TGCGTAGCAG	CCACACTGCT	GGTGGCTGAG	GAGGCAGCAG	TGGGCCCCAC	960
CGAGCCAGCA	GAAGGGCTGT	CGGCCCCCTC	CTTGTGCC	CACTGCTGTC	CATGCCGGC	1020
CCGCTTGGCT	TTCCGGAACC	TGGCGCCCT	GCTTCCC	CTGCACCAGC	TGTGCTGCCG	1080
CATGCCCGC	ACCCCTGCGC	GGCTCTTCGT	GGCTGAGCTG	TGCACTGGA	TGGCACTCAT	1140
GACCTTCACG	CTGTTTTACA	CGGATTTCTG	GGGCGAGGGG	CTGTACCAGG	CGGTGCCAG	1200
AGCTGAGCCG	GGCACCCGAGG	CCCGGAGACCA	CTATGATGAA	GGCGTTCGGA	TGGCAGCCT	1260
GGGGCTGTT	CTGCACTGCG	CCATCTCCCT	GGTCTCTCT	CTGGTCATGG	ACCGGCTGGT	1320
GCAGCGATT	GGCACTCGAG	CAGTCTATT	GGCCAGTGTG	GCAGCTTCC	CTGTGGCTGC	1380
CGGTGCCACA	TGCTGTCCC	ACAGTGTGGC	CGTGGTGACA	GCTTCAGCCG	CCCTCACCGG	1440
GTTCACCTTC	TCAGCCCTGC	AGATCCTGCC	CTACACACTG	GCCTCCCTCT	ACCACCGGA	1500
GAAGCAGGTG	TTCTGCCCA	AATACCGAGG	GGACACTGGA	GGTGTAGCA	GTGAGGACAG	1560
CCTGATGACC	AGCTTCCCTGC	CAGGCCCTAA	GCCTGGAGCT	CCCTTCCCTA	ATGGACACGT	1620
GGGTGCTGGA	GGCAGTGGCC	TGCTCCCACC	TCCACCCCG	CTCTGCGGGG	CCTCTGCTG	1680
TGATGTCTCC	GTACGTGTGG	TGGTGGGTGA	GCCCACCGAG	GCCAGGGTGG	TTCCGGCCG	1740
GGGCATCTGC	CTGGACCTCG	CCATCTGG	TAGTGCCTTC	CTGCTGTCCC	AGGTGGCCCC	1800
ATCCCTGTTT	ATGGGCTCCA	TTGTCAGCT	CAGCCAGTCT	GTCACTGCC	ATATGGTGT	1860
TGCCGAGGC	CTGGGCTCTGG	TCGCCATT	CTTGCTACA	CAGGTAGTAT	TTGACAAGAG	1920
CGACTTGGCC	AAATACTCAG	CGTAGAAAAC	TTCCAGCACA	TTGGGGTGG	GGGCCTGCC	1980
CACTGGGTCC	CAGCTCCCCG	CTCCCTGTTAG	CCCCATGGGG	CTGCCGGGCT	GGCCGCCAGT	2040
TTCTGTTGCT	GCCAAAGTAA	TGTGGCTCTC	TGCTGCCACC	CTGTGCTGCT	GAGGTGCGTA	2100
GCTGCACAGC	TGGGGCTGG	GGCGTCCCTC	TCCTCTCTCC	CCAGTCTCTA	GGGCTGCTG	2160
ACTGGAGGCC	TTCCAAGGGG	GTTCAAGTCT	GGACTTATAC	AGGGAGGCCA	GAAGGGCTCC	2220
ATGCACTGGA	ATGCGGGGAC	TCTGCAGGTG	GATTACCCAG	GCTCAGGGTT	AACAGCTAGC	2280
CTCCTAGTTG	AGACACACCT	AGAGAAGGGT	TTTTGGGAGC	TGAATAAACT	CAGTCACCTG	2340
GTTTCCCACATC	TCTAACCCCC	TTAACCTGCA	GCTTCGTTA	ATGTAGCTCT	TGCATGGGAG	2400
TTTCTAGGAT	GAAACACTCC	TCCATGGGAT	TTGAACATAT	GACTTATTG	TAGGGGAAGA	2460

GTCCTGAGGG GCAACACACA AGAACCCAGGT CCCCTCAGCC CACAGCACTG TCTTTTGCT	2520
GATCCACCCC CCTCTTACCT TTTATCAGGA TGTGGCCTGT TGGTCCTTCT GTGCCATCA	2580
CAGAGACACA GGCATTTAAA TATTTAACTT ATTTATTTAA CAAAGTAGAA GGGATCCAT	2640
TGCTAGCTT TCTGTGTTGG TGTCTAATAT TTGGGTAGGG TGCGGGATCC CCAACAATCA	2700
GGTCCCTGA GATAGCTGGT CATTGGGCTG ATCATTGCCA GAATCTTCTT CTCCTGGGT	2760
CTGGCCCCCC AAAATGCCA ACCCAGGACC TTGGAAATTCT TACTCATCCC AAATGATAAT	2820
TCCAATGCT GTTACCAAG GTAGGGTGT TGAAGGAAGG TAGAGGGTGG GGCTTCAGGT	2880
CTCAACGGCT TCCCTAACCA CCCCTCTTCT CTTGGCCAG CCTGGTTCCC CCCACTCCA	2940
CTCCCCCTCA CTCTCTCTAG GACTGGGCTG ATGAAGGCAC TGCCCAAAT TTCCCCCTACC	3000
CCCAACTTTC CCCTACCCCCC AACTTTCCCC ACCAGCTCCA CAACCTGTT TGGAGCTACT	3060
GCAGGACCAAG AAGCACAAAG TGCGGTTTC CAAGCCTTTG TCCATCTCAG CCCCCAGAGT	3120
ATATCTGTGC TTGGGAATC TCACACAGAA ACTCAGGAGC ACCCCCTGCC TGAGCTAAGG	3180
GAGGTCTTAT CTCTCAGGGG GGTTTAAGT GCCGTTGCA ATAATGTCGT CTTATTATT	3240
TAGCGGGGTG AATATTTAT ACTGTAAGTG AGCAATCAGA GTATAATGTT TATGGTGACA	3300
AAATTAAAGG CTTTCTTATA TGTTAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	3360
AAAAAAAAAA AAAAAAAAAA AAAAAAATAA AAAAAAAAAA	3410

## (2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

AGCCAGGCGT CCCTCTGCCT GCCCACTCAG TGGCAACACC CGGGAGCTGT TTTGTCTTT	60
GTGGAGCCTC AGCAGTTCCC TCTTCAGAA CTCACTGCCA AGAGCCCTGA ACAGGAGCCA	120
CCATGCAGTG CTTCAGCTTC ATTAAGACCA TGATGATCCT CTTCAATTG CTCATCTTC	180
TGTGTGGTGC AGCCCTGTTG GCAGTGGGCA TCTGGGTGTC AATCGATGGG GCATCCTTC	240
TGAAGATCTT CGGGCCACTG TCGTCCAGTG CCATGCAGTT TGTCAACGTG GGCTACTTCC	300
TCATCGCAGC CGGCCTTGTG GTCTTGTCT TTGGTTCCCT GGGCTGCTAT GGTGCTAAGA	360
CTGAGAGCAA GTGTGCCCTC GTGACGTTCT TCTTCATCCT CCTCCTCATC TTCATTGCTG	420
AGGTTGCAGC TGCTGTGGTC GCCTTGGTGT ACACCACAT GGCTGACCAC TTCCTGACGT	480
TGCTGGTAGT GCCTGCCATC AAGAAAGATT ATGGTTCCA GGAAGACTTC ACTCAAGTGT	540
GGAACACCCAC CATGAAAGGG CTCAGTGCT GTGGCTTCAC CAACTATACG GATTTGAGG	600
ACTCACCCATA CTTCAAAGAG AACAGTGCCT TTCCCCCATT CTGTTGCAAT GACAACGTCA	660
CCAACACAGC CAATGAAACC TGACCAAGC AAAAGGCTCA CGACCAAAAA GTAGAGGGTT	720
GCTTCAATCA GCTTTGTAT GACATCCGAA CTAATGCACT CACCGTGGGT GGTGTGGCAG	780
CTGGAATTGG GGGCCTCGAG CTGGCTGCCA TGATTGTGTC CATGTATCTG TACTGCAATC	840
TACAATAAGT CCACTCTGC CTCTGCCACT ACTGCTGCCA CATGGGAACT GTGAAGAGGC	900
ACCCTGGCAA GCAGCAGTGA TTGGGGGAGG GGACAGGATC TAACAATGTC ACTTGGCCA	960
GAATGGACCT GCCCTTCTG CTCCAGACTT GGGGCTAGAT AGGGACCACT CCTTTTAGCG	1020
ATGCCTGACT TTCCCTCCAT TGTTGGGTGG ATGGGTGGGG GGCATTCCAG AGCCTCTAAG	1080
GTAGCCAGTT CTGTTGCCCA TTCCCCCAGT CTATTAACC CTTGATATGC CCCCTAGGCC	1140
TAGTGGTGAT CCCAGTGCTC TACTGGGGGA TGAGAGAAAG GCATTTATA GCCTGGCAT	1200
AAGTGAATC AGCAGAGCCT CTGGGTGGAT GTGTAGAAGG CACTTCAAAA TGCATAAACC	1260
TGTTACAATG TTAAAAAAA AAAAAAAAAA	1289

## (2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Met Val Phe Thr Val Arg Leu Leu His Ile Phe Thr Val Asn Lys Gln  
1 5 10 15

Leu Gly Pro Lys Ile Val Ile Val Ser Lys Met Met Lys Asp Val Phe  
20 25 30

Phe Phe Leu Phe Phe Leu Gly Val Trp Leu Val Ala Tyr Gly Val Ala  
35 40 45

Thr Glu Gly Leu Leu Arg Pro Arg Asp Ser Asp Phe Pro Ser Ile Leu  
50 55 60

Arg Arg Val Phe Tyr Arg Pro Tyr Leu Gln Ile Phe Gly Gln Ile Pro  
65 70 75 80

Gln Glu Asp Met Asp Val Ala Leu Met Glu His Ser Asn Cys Ser Ser  
85 90 95

Glu Pro Gly Phe Trp Ala His Pro Pro Gly Ala Gln Ala Gly Thr Cys  
100 105 110

Val Ser Gln Tyr Ala Asn Trp Leu Val Val Leu Leu Val Ile Phe  
115 120 125

Leu Leu Val Ala Asn Ile Leu Leu Val Asn Leu Leu Ile Ala Met Phe  
130 135 140

Ser Tyr Thr Phe Gly Lys Val Gln Gly Asn Ser Asp Leu Tyr Trp Lys  
145 150 155 160

Ala Gln Arg Tyr Arg Leu Ile Arg Glu Phe His Ser Arg Pro Ala Leu  
165 170 175

Ala Pro Pro Phe Ile Val Ile Ser His Leu Arg Leu Leu Arg Gln  
180 185 190

Leu Cys Arg Arg Pro Arg Ser Pro Gln Pro Ser Ser Pro Ala Leu Glu  
195 200 205

His Phe Arg Val Tyr Leu Ser Lys Glu Ala Glu Arg Lys Leu Thr

210

215

220

Trp Glu Ser Val His Lys Glu Asn Phe Leu Leu Ala Arg Ala Arg Asp  
 225 230 235 240

Lys Arg Glu Ser Asp Ser Glu Arg Leu Lys Arg Thr Ser Gln Lys Val  
 245 250 255

Asp Leu Ala Leu Lys Gln Leu Gly His Ile Arg Glu Tyr Glu Gln Arg  
 260 265 270

Leu Lys Val Leu Glu Arg Glu Val Gln Gln Cys Ser Arg Val Leu Gly  
 275 280 285

Trp Val Ala Glu Ala Leu Ser Arg Ser Ala Leu Leu Pro Pro Gly Gly  
 290 295 300

Pro Pro Pro Pro Asp Leu Pro Gly Ser Lys Asp  
 305 310 315

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 553 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala  
 1 5 10 15

Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu  
 20 25 30

Ala Ala Gly Ile Thr Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val  
 35 40 45

Glu Glu Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly  
 50 55 60

Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly  
 65 70 75 80

Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile  
 85 90 95

Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu  
 100 105 110

Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Ile Leu Gly  
 115 120 125  
 Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu  
 130 135 140  
 Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala  
 145 150 155 160  
 Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr  
 165 170 175  
 Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu  
 180 185 190  
 Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu  
 195 200 205  
 Thr Cys Val Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly  
 210 215 220  
 Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His  
 225 230 235 240  
 Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu  
 245 250 255  
 Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg  
 260 265 270  
 Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe  
 275 280 285  
 Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Leu Tyr Gln Gly Val  
 290 295 300  
 Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly  
 305 310 315 320  
 Val Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu  
 325 330 335  
 Val Phe Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg  
 340 345 350  
 Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala  
 355 360 365  
 Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu  
 370 375 380  
 Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala  
 385 390 395 400

Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly  
 405 410 415  
 Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu  
 420 425 430  
 Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala  
 435 440 445  
 Gly Gly Ser Gly Leu Leu Pro Pro Pro Ala Leu Cys Gly Ala Ser  
 450 455 460  
 Ala Cys Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala  
 465 470 475 480  
 Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp  
 485 490 495  
 Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser  
 500 505 510  
 Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala  
 515 520 525  
 Gly Leu Gly Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp  
 530 535 540  
 Lys Ser Asp Leu Ala Lys Tyr Ser Ala  
 545 550

## (2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu  
 1 5 10 15  
 Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val  
 20 25 30  
 Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser  
 35 40 45  
 Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly

90

50	55	60
Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr		
65	70	75
Glu Ser Lys Cys Ala Leu Val Thr Phe Phe Phe Ile Leu Leu Leu Ile		
85	90	95
Phe Ile Ala Glu Val Ala Ala Val Val Ala Leu Val Tyr Thr Thr		
100	105	110
Met Ala Glu His Phe Leu Thr Leu Leu Val Val Pro Ala Ile Lys Lys		
115	120	125
Asp Tyr Gly Ser Gln Glu Asp Phe Thr Gln Val Trp Asn Thr Thr Met		
130	135	140
Lys Gly Leu Lys Cys Cys Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp		
145	150	155
Ser Pro Tyr Phe Lys Glu Asn Ser Ala Phe Pro Pro Phe Cys Cys Asn		
165	170	175
Asp Asn Val Thr Asn Thr Ala Asn Glu Thr Cys Thr Lys Gln Lys Ala		
180	185	190
His Asp Gln Lys Val Glu Gly Cys Phe Asn Gln Leu Leu Tyr Asp Ile		
195	200	205
Arg Thr Asn Ala Val Thr Val Gly Gly Val Ala Ala Gly Ile Gly Gly		
210	215	220
Leu Glu Leu Ala Ala Met Ile Val Ser Met Tyr Leu Tyr Cys Asn Leu		
225	230	235
Gln		

## (2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GCTCTTCCTC TCCCCTCCTC TGAATTTAAT TCTTTCAACT TGCAATTGC AAGGATTACA	60
CATTTCACTG TGATGTATAT TGTGTTGCAA AAAAAAAA GTGCTTTGT TTAAAATTAC	120
TTGGTTTGTG AATCCATCTT GCTTTTCCC CATTGGAAC ACTCATTAAC CCATCTCTGA	180
ACTGGTAGAA AAACATCTGA AGAGCTAGTC TATCAGCAG TGACAGGTGA ATTGGATGGT	240
TCTCAGAACC ATTTCACCCCA GACAGCCTGT TTCTATCCTG TTTAATAAT TAGTTGGGT	300
TCTCTACATG CATAACAAAC CCTGCTCCAA TCTGTACAT AAAAGTCTGT GACTTGAACT	360
TTAGTC	366

## (2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

ACAAAGATGA ACCATTTCCT ATATTATAGC AAAATTAAAA TCTACCCGTA TTCTAATATT	60
GAGAAATGAG ATNAAACACA ATNTTATAAA GTCTACTTAG AGAAGATCAA GTGACCTCAA	120
AGACTTTACT ATTTTCATAT TTTAAGACAC ATGATTATTC CTATTTAGT AACCTGGTTC	180
ATACGTTAAA CAAAGGATAA TGTGAACAGC AGAGAGGATT TGTGGCAGA AAATCTATGT	240
TCAATCTNGA ACTATCTANA TCACAGACAT TTCTATTCCCT TT	282

## (2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

ACACATGTCG CTTCACTGCC TTCTTAGATG CTTCTGGTCA ACATANAGGA ACAGGGACCA	60
TATTTATCCT CCCTCCTGAA ACAATTGCAA AATAANACAA AATATATGAA ACAATTGCAA	120
AATAAGGCAA AATATATGAA ACAACAGGTC TCGAGATATT GGAAATCAGT CAATGAAGGA	180
TACTGATCCC TGATCACTGT CCTAATGCAAG GATGTGGGAA ACAGATGAGG TCACCTCTGT	240
GACTGCCCA GCTTACTGCC TGTAGAGAGT TTCTANGCTG CAGTCAGAC AGGGAGAAAT	300
TGGGT	305

## (2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

ACCAAGGTGT NTGAATCTCT GACGTGGGGA TCTCTGATTC CCGCACAAATC TGAGTGGAAA 60  
AANTCCTGGG T 71

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

ACTCCGGTTG GTGTCAGCAG CACGTGGCAT TGAACATNGC AATGTGGAGC CCAAACCAACA 60  
GAAAATGGGG TGAAATTGGC CAACTTTCTA TNAACTTATG TTGGCAANTT TGCCACCAAC 120  
AGTAAGCTGG CCCTTCTAAT AAAAGAAAAT TGAAAGGTTT CTCACTAANC GGAATTAANT 180  
AATGGANTCA AGANACTCCC AGGCCTCAGC GT 212

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

ACTCGTTGCA NATCAGGGGC CCCCCAGAGT CACCGTTGCA GGAGTCCTTC TGGTCTTGCC 60  
CTCCGCCGGC GCAGAACATG CTGGGGTGGT 90

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

TGTANCAGA ANACGACAGA NAGGGTTGTC AAAAATGGAG AANCTTGAA GTCATTTGA	60
GAATAAGATT TGCTAAAAGA TTTGGGGCTA AAACATGGTT ATTGGGAGAC ATTTCTGAAG	120
ATATNCANGT AAATTANGGA ATGAATTCTAT GGTTCTTTG GGAATTCCCT TACGATNGCC	180
AGCATANACT TCATGTGGGG ATANCAGCTA CCCTTGTA	218

(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

TAGGGGTGTA TGCAACTGTA AGGACAAAAA TTGAGACTCA ACTGGCTTAA CCAATAAAGG	60
CATTGTTAG CTCATGGAAC AGGAAGTCGG ATGGTGGGGC ATCTTCAGTG CTGCATGAGT	120
CACCACCCCG GCGGGGTCACT GTGTGCCACA GGTCCCTGTT GACAGTGCAGG T	171

(2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 76 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

TGTAGCGTGA AGACNACAGA ATGGTGTGTG CTGTGCTATC CAGGAACACA TTTATTATCA	60
TTATCAANTA TTGTGT	76

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 131 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

ACCTTTCCCC AAGGCCAATG TCCTGTGTGC TAACTGGCCG GCTGCAGGAC AGCTGCAATT 60  
 CAATGTGCTG GGTCAATATGG AGGGGGAGGAG ACTCTAAAAT AGCCAATT TT ATTCTCTTGG 120  
 TTAAGATTG T 131

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 432 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

ACTTTATCTA CTGGCTATGA AATAGATGGT GGAAAATTGC GTTACCAACT ATACCACTGG 60  
 CTTGAAAAAG AGGTGATAGC TCTTCAGAGG ACTTGTGACT TTTGCTCAGA TGCTGAAGAA 120  
 CTACAGTCTG CATTGGCAG AAATGAAGAT GAATTGGAT TAAATGAGGA TGCTGAAGAT 180  
 TTGCCTCACCC AAACAAAAGT GAAACAACTG AGAGAAAATT TTCAGGAAAA AAGACAGTGG 240  
 CTCTTGAAGT ATCAGTCACT TTTGAGAATG TTTCTTAGTT ACTGCATACT TCATGGATCC 300  
 CATGGTGGGG GTCTTGCATC TGTAAGAATG GAATTGATT TGCTTTGCA AGAATCTCAG 360  
 CAGGAAACAT CAGAACCACT ATTTTCTAGC CCTCTGTCAG AGCAAAACCTC AGTGCCTCTC 420  
 CTCTTGCTT GT 432

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 112 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

ACACAACCTG AATAGAAAAA TAGAAACTGA GCTGAAATTT CTAATTCACT TTCTAACCAT	60
AGTAAGAATG ATATTTCCCC CCAGGGATCA CCAAATATTT ATAAAAAATTT GT	112

## (2) INFORMATION FOR SEQ ID NO:127:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

ACCACGAAAC CACAAACAAG ATGGAAGCAT CAATCCACTT GCCAAGCACA GCAG	54
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## (2) INFORMATION FOR SEQ ID NO:128:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

ACCTCATTAG TAATTGTTTT GTTGTTCAT TTTTTCTAA TGCTCTCCCT CTACCAGCTC	60
ACCTGAGATA ACAGAATGAA AATGGAAGGA CAGCCAGATT TCTCCTTTGC TCTCTGCTCA	120
TTCTCTCTGA AGTCTAGGTT ACCCATTGG GGGACCCATT ATAGGCAATA AACACAGTTC	180
CCAAAGCATT TGGACAGTTT CTTGTTGTGT TTTAGAATGG TTTCCCTTT TCTTAGCCTT	240
TTCCTGAAA AGGCTCACTC AGTCCCTTGC TTGCTCAGTG GACTGGGCTC CCCAGGGCCT	300
AGGCTGCCTT CTTTCCATG TCC	323

## (2) INFORMATION FOR SEQ ID NO:129:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

ACATACATGT GTGTATATT TTAAATATCA CTTTTGTATC ACTCTGACTT TTTAGCATA	60
TGAAAACACA CTAACATAAT TTNTGTGAAC CATGATCAGA TACAACCCAA ATCATTCA	120
TAGCACATTC ATCTGTGATA NAAAGATAGG TGAGTTCAT TTCCTTCACG TTGGCCAATG	180
GATAAACAAA GT	192

## (2) INFORMATION FOR SEQ ID NO:130:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

CCCTTTTTA TGGAATGAGT AGACTGTATG TTTGAANATT TANCCACAAAC CTCTTTGACA	60
TATAATGACG CAAACAAAAG GTGCTTTA GTCCTATGGT TCAGTTTATG CCCCTGACAA	120
GTITCCATTG TGTTTGCCG ATCTTCTGGC TAATCGTGGT ATCCTCCATG TTATTAGTAA	180
TTCTGTATTC CATTGGTTA ACGCCTGGT AATGTAACCT GCTANGAGGC TAACTTTATA	240
CTTATTTAAA AGCTCTTATT TTGTGGTCAT TAAAATGGCA ATTATATGTGC AGCACTTTAT	300
TGCAGCAGGA AGCACGTGTG GGTTGGTTGT AAAGCTCTT GCTAATCTTA AAAAGTAATG	360
GG	362

## (2) INFORMATION FOR SEQ ID NO:131:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

CTTTTGAAA GATCGTGTCC ACTCCTGTGG ACATCTTGT TTAATGGAGT TTCCCATGCA	60
GTANGACTGG TATGGTTGCA GCTGTCCAGA TAAAAACATT TGAAGAGCTC CAAAATGAGA	120
GTTCTCCAG GTTCGCCCTG CTGCTCCAAG TCTCAGCAGC AGCCTCTTTT AGGAGGCATC	180
TTCTGAACTA GATTAAGGCA GCTTGTAAAT CTGATGTGAT TTGGTTTATT ATCCAACCAA	240
CTTCCATCTG TTATCACTGG AGAAAGCCCA GACTCCCCAN GACNGGTACG GATTGTGGC	300
ATANAAGGAT TGGGTGAAGC TGGCGTTGTG GT	332

## (2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 322 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

ACTTTGCCA	TTTTGTATAT	ATAAACAAATC	TTGGGACATT	CTCCTGAAAA	CTAGGTGTCC	60
AGTGGCTAAG	AGAACTCGAT	TTCAAGCAAT	TCTGAAAGGA	AAACCAGCAT	GACACAGAAT	120
CTCAAATTCC	CAAACAGGGG	CTCTGTGGGA	AAAATGAGGG	AGGACCTTG	TATCTCGGGT	180
TTTAGCAAGT	TAAAATGAAN	ATGACAGGAA	AGGCTTATTT	ATCAACAAAG	AGAAGAGTTG	240
GGATGCTTCT	AAAAAAAACT	TTGGTAGAGA	AAATAGGAAT	GCTNAATCCT	AGGGAAGCCT	300
GTAACAATCT	ACAATTGGTC	CA				322

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 278 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

ACAAGCCTTC	ACAAGTTAA	CTAAATTGGG	ATTAATCTTT	CTGTANTTTAT	CTGCATAATT	60
CTTGTGTTTC	TTTCCATCTG	GCTCCTGGGT	TGACAATTG	TGGAAACAAC	TCTATTGCTA	120
CTATTTAAAA	AAAATCACAA	ATCTTCCCT	TTAACGCTATG	TTNAATTCAA	ACTATTCCG	180
CTATTCCGT	TTTGTCAAAG	AAATTATATT	TTTCAAAATA	TGTNTATTG	TTTGATGGGT	240
CCACGAAAC	ACTAATAAAA	ACCACAGAGA	CCAGCCTG			278

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 121 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GTTTANAAAA CTTGTTAGC TCCATAGAGG AAAGAATGTT AAACTTTGTA TTTTAAAACA	60
TGATTCTCTG AGGTTAAACT TGTTTTCAA ATGTTATTT TACTTGTATT TTGCTTTGG	120
T	121

## (2) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 350 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *Homo sapiens*

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

ACTTANAAACC ATGCCTAGCA CATCAGAACATC CCTCAAAGAA CATCAGTATA ATCCCTATACC	60
ATANCAAGTG GTGACTGGTT AAGCGTGCAG CAAAGGTCAG CTGGCACATT ACTTGTGTGC	120
AAACTTGATA CTTTTGTTCT AAGTAGGAAC TAGTATACAG TNCTAGGAN TGGTACTCCA	180
GGGTGCCCCC CAACTCCTGC AGCCGCTCCT CTGTGCCAGN CCCTGNAAGG AACTTTCGCT	240
CCACCTCAAT CAAGCCCTGG GCCATGCTAC CTGCAATTGG CTGAACAAAC GTTGCTGAG	300
TTCCCAAGGA TGCAAAGCCT GGTGCTCAAC TCCTGGGGCG TCAACTCAGT	350

## (2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 399 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *Homo sapiens*

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

TGTACCGTGA AGACGACAGA AGTTGCATGG CAGGGACAGG GCAGGGCCGA GGCCAGGGTT	60
GCTGTGATTG TATCGAATA NTCCTCGTGA GAAAAGATAA TGAGATGACG TGAGCAGCCT	120
GCAGACTTGT GTCTGCCTTC AANAAGCCAG ACAGGAAGGC CCTGCCTGCC TTGGCTCTGA	180
CCTGGCGGCC AGCCAGCCAG CCACAGGTGG GCTTCTCCT TTTGTGGTGA CAACNCCAAG	240
AAAATGCAG AGGCCAGGG TCAGGTGTNA GTGGGTANGT GACCATAAAA CACCAGGTGC	300
TCCCAGGAAC CGGGGCAAAG GCCATCCCCA CCTACAGCCA GCATGCCAC TGGCGTGATG	360
GGTGCAGANG GATGAAGCAG CCAGNTGTTC TGCTGTGGT	399

## (2) INFORMATION FOR SEQ ID NO:137:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 165 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

ACTGGTGTGG TNGGGGGTGA TGCTGGTGGT ANAAGTTGAN GTGACTTCAN GATGGTGTGT	60
GGAGGAAGTG TGTGAACGTA GGGATGTAGA NGTTTGGCC GTGCTAAATG AGCTTCGGGA	120
TTGGCTGGTC CCACTGGTGG TCACTGTCAT TGGTGGGGTT CCTGT	165

(2) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

ACTCACTGGA ATGCCACATT CACAAACAGAA TCAGAGGGTCT GTGAAAACAT TAATGGCTCC	60
TTAACCTCTC CAGTAAGAAT CAGGGACTTG AAATGGAAAC GTTAAACAGCC ACATGCCAA	120
TGCTGGCAG TCTCCCAGTC CTTCCACAGT GAAAGGGCTT GAGAAAAATC ACATCCAATG	180
TCATGTGTTT CCAGCCACAC CAAAAGGTGC TTGGGGTGGGA GGGCTGGGGG CATANANGGT	240
CANGCCTCAG GAAGCCTCAA GTTCCATTCA GCTTGCACAC TGTACATTCC CCATNTTAA	300
AAAAACTGAT GCCTTTTTT TTTTTTTTG TAAAATTTC	338

(2) INFORMATION FOR SEQ ID NO:139:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 382 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GGGAATCTTG GTTTTGGCA TCTGGTTGCT ATAGCCGA GGCCACTTTG ACAGAACAAA	60
GAAAGGGACT TCGAGTAAGA AGGTGATTAA CAGCCAGCCT AGTGCCCCAA GTGAAGGAGA	120
ATTCAAACAG ACCTCGTCAT TCCTGGTGTG AGCCTGGTCG GCTCACCGCC TATCATCTGC	180

100

ATTTGCCTTA CTCAGGTGCT ACCGGACTCT GGCCCTGAT GTCTGTAGTT TCACAGGATG	240
CCTTATTTGT CTTCTACACC CCACAGGGCC CCCTACTTCT TCGGATGTGT TTTTAATAAT	300
GTCAGCTATG TGCCCCATCC TCCTTCATGC CCTCCCTCCC TTTCCTACCA CTGCTGAGTG	360
GCCTGGAACT TGTAAAGT GT	382

## (2) INFORMATION FOR SEQ ID NO:140:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 200 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

ACCAAANCTT CTTTCTGTTG TGTNGATTT TACTATAGGG GTTTNGCTTN TTCTAAANAT	60
ACTTTTCATT TAACANCTTT TGTTAAGTGT CAGGCTGCAC TTTGCTCCAT ANAATTATTG	120
TTTTCACATT TCAACTTGTA TGTGTTGTC TCTTANAGCA TTGGTGAAT CACATATTAA	180
ATATTCAAGCA TAAAGGAGAA	200

## (2) INFORMATION FOR SEQ ID NO:141:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 335 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

ACTTTATTTT CAAAACACTC ATATGTTGCA AAAAACACAT AGAAAAATAA AGTTTGGTGG	60
GGGTGCTGAC TAAACTTCAA GTCACAGACT TTTATGTGAC AGATTGGAGC AGGGTTGTGTT	120
ATGCATGTAG AGAACCCAAA CTAATTTATT AAACAGGATA GAAACAGGCT GTCTGGGTGA	180
AATGGTTCTG AGAACCATCC AATTCACTTG TCAGATGCTG ATANACTAGC TCTTCAGATG	240
TTTTTCTACC AGTCAGAGA TNGGTTAATG ACTANTTCCA ATGGGGAAAA AGCAAGATGG	300
ATTCAACAAAC CAAGTAATTT TAAACAAAGA CACTT	335

## (2) INFORMATION FOR SEQ ID NO:142:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 459 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

ACCAGGTTAA TATTGCCACA TATATCCTT CCAATTGCGG GCTAACAGA CGTGTATTTA	60
GGGTTGTTA AAGACAACCC AGCTTAATAT CAAGAGAAAT TGTGACCTTT CATGGAGTAT	120
CTGATGGAGA AAACACTGAG TTTTGACAAA TCTTATTTA TTCAGATAGC AGTCTGATCA	180
CACATGGTCC ACAACACACTC AAATAATAAA TCAAATATNA TCAGATGTTA AAGATTGGTC	240
TTCAAACATC ATAGCCAATG ATGCCCGCT TGCCTATAAT CTCTCCGACA TAAAACCACA	300
TCAACACCTC AGTGGCCACC AAACCATTCA GCACAGCTTC CTTAACTGTG AGCTGTTGA	360
AGCTACCACTG CTGAGCACTA TTGACTATNT TTTTCANGCT CTGAATAGCT CTAGGGATCT	420
CAGCANGGGT GGGAGGAACC AGCTAACCT TGGCGTANT	459

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

ACATTTCTT CCACCAAGTC AGGACTCCTG GCTTCTGTGG GAGTTCTTAT CACCTGAGGG	60
AAATCCAAAC AGTCTCTCCT AGAAAGGAAT AGTGTACCA ACCCCACCA TCTCCCTGAG	120
ACCATCCGAC TTCCCTGTGT	140

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

ACTTCAGTAA CAACATACAA TAACAAACATT AAGTGTATAT TGCCATCTT GTCATTTCT	60
ATCTATACCA CTCTCCCTTC TGAAAACAAN AATCACTANC CAATCACTTA TACAAATTG	120
AGGCAATTAA TCCATATTG TTTTCATAAA GGAAAAAAAG ATGT	164

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 303 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

ACGTAGACCA TCCAACTTTG TATTGTAAAT GGCAAACATC CAGNAGCAAT TCCTAAACAA	60
ACTGGAGGGT ATTTATACCC AATTATCCCA TTCATTAACA TGCCCTCCTC CTCAGGCTAT	120
GCAGGACAGC TATCATAAGT CGGCCAGGC ATCCAGATAC TACCATTGTG ATAAACTTCA	180
GTAGGGGAGT CCATCCAAGT GACAGGTCTA ATCAAAGGAG GAAATGGAAC ATAAGCCAG	240
TAGTAAAATN TTGCTTAGCT GAAACAGCCA CAAAAGACTT ACCGCCGTGG TGATTACCAT	300
CAA	303

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 327 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

ACTGCAGCTC AATTAGAAAGT GGTCTCTGAC TTTCATCANC TTCTCCCTGG GCTCCATGAC	60
ACTGGCCTGG AGTGACTCAT TGCTCTGGTT GGTTGAGAGA GCTCCTTGC CAACAGGCCT	120
CCAAGTCAGG GCTGGGATTT GTTCCCTTTC CACATTCTAG CAACAATATG CTGGCCACTT	180
CCTGAACAGG GAGGGTGGGA GGAGCCAGCA TGGAACAAGC TGCCACTTTC TAAAGTAGCC	240
AGACTTGCCTT CTGGCCCTGT CACACCTACT GATGACCTTC TGTGCCTGCA GGATGGAATG	300
TAGGGGTGAG CTGTGTGACT CTATGGT	327

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 173 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Homo sapiens*

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

ACATTGTTTT TTTGAGATAA AGCATTGANA GAGCTCTCCT TAACGTGACA CAATGGAAGG	60
ACTGGAACAC ATACCCACAT CTTTGTCTG AGGGATAATT TTCTGATAAA GTCTTGCTGT	120
ATATTCAAGC ACATATGTTA TATATTATTC AGTTCCATGT TTATAGCCTA GTT	173

## (2) INFORMATION FOR SEQ ID NO:148:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

ACAACCACCTT TATCTCATCG AATTTTAAC CCAAACCTCAC TCACTGTGCC TTTCTATCCT	60
ATGGGATATA TTATTTGATG CTCCATTCA TCACACATAT ATGAATAATA CACTCATACT	120
GCCCTACTAC CTGCTGCAAT AATCACATTC CCTTCCTGTC CTGACCCCTGA AGCCATTGGG	180
GTGGTCTCTAG TGGCCATCAG TCCANGCCTG CACCTTGAGC CCTTGAGCTC CATTGCTCAC	240
NCCANCCAC CTCACCGACC CCATCCTCTT ACACAGCTAC CTCCTTGCTC TCTAACCCCA	300
TAGATTATNT CCAAATTCAAG TCAATTAAGT TACTATTAAC ACTCTACCCG ACATGTCCAG	360
CACCACTGGT AAGCCTTCTC CAGCCAACAC ACACACACAC ACACNCACAC ACACACATAT	420
CCAGGCACAG GCTACCTCAT CTTCACAAATC ACCCCTTTAA TTACCATGCT ATGGTGG	477

## (2) INFORMATION FOR SEQ ID NO:149:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

ACAGTTGTAT TATAATATCA AGAAATAAAC TTGCAATGAG AGCATTAAAG AGGGAAGAAC	60
TAACGTATTT TAGAGGCCA AGGAAGGTTT CTGTGGGGAG TGGGATGTAA GGTGGGGCCT	120
GATGATAAT AAGAGTCAGC CAGGTAAGTG GGTGGTGTGG TATGGGCACA GTGAAGAACAA	180
TTTCAGGCAG AGGGAACAGC AGTGAAGA	207

## (2) INFORMATION FOR SEQ ID NO:150:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

ACCTTGATTT CATTGCTGCT CTGATGGAAA CCCAACTATC TAATTTAGCT AAAACATGGG 60  
CACTTAAATG TGGTCAGTGT TTGGACTTGT TAACTANTGG CATCTTTGGG T 111

(2) INFORMATION FOR SEQ ID NO:151:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 196 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

AGCGCGGCAG GTCATATTGA ACATTCCAGA TACCTATCAT TACTCGATGC TGTTGATAAC 60  
AGCAAGATGG CTTTGAACTC AGGGTCACCA CCAGCTATTG GACCTTACTA TGAAAACCAT 120  
GGATACCAAC CGGAAAACCC CTATCCGCA CAGCCCCTG TGGTCCCCAC TGTCTACGAG 180  
GTGCATCCGG CTCAGT 196

(2) INFORMATION FOR SEQ ID NO:152:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

ACAGCACTTT CACATGTAAG AAGGGAGAAA TTCCTAAATG TAGGAGAAAG ATAACAGAAC 60  
CTTCCCCTTT TCATCTAGTG GTGGAAACCT GATGCTTTAT GTTGACAGGA ATAGAACCG 120  
GAGGGAGTTT GT 132

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 285 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

ACAAANACCCA	NGANAGGCCA	CTGGCCGTGG	TGTCATGGCC	TCCAAACATG	AAAGTGTAG	60
CTTCTGCTCT	TATGTCCTCA	TCTGACAACT	CTTTACCATT	TTTATCCTCG	CTCAGCAGGA	120
GCACATCAAT	AAAGTCCAAA	GTCTTGGACT	TGGCCTTGGC	TTGGAGGAAG	TCATCAACAC	180
CCTGGCTAGT	GAGGGTGCAG	CGCCGCTCCT	GGATGACGGC	ATCTGTGAAG	TCGTGCACCA	240
GTCTGCAGGC	CCTGTGGAAG	CGCCGTCAC	ACGGAGTNAG	GAATT		285

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 333 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

ACCACAGTCC	TGTTGGGCCA	GGGCTTCATG	ACCCTTTCTG	TGAAAAGCCA	TATTATCACC	60
ACCCCAAATT	TTTCCTTAAA	TATCTTAAAC	TGAAGGGGTC	AGCCTCTTGA	CTGCAAAGAC	120
CCTAAGCCGG	TTACACAGCT	AACTCCCCT	GGCCCTGATT	TGTGAAATTG	CTGCTGCCTG	180
ATTGGCACAG	GAGTCGAAGG	TGTCAGCTC	CCCTCCTCCG	TGGAACGAGA	CTCTGATTTG	240
AGTTTCACAA	ATTCTCGGGC	6ACCTCGTCA	TTGCTCCTCT	GAAATAAAAT	CCGGAGAATG	300
GTCAGGCCTG	TCTCATCCAT	ATGGATCTTC	CGG			333

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 308 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

ACTGGAAATA ATAAAACCCA CATCACAGTG TTGTGTCAA GATCATCAGG GCATGGATGG	60
GAAAGTGCTT TGGGAACGTG AAAGTGCCTA ACACATGATC GATGATTTTT GTTATAATAT	120
TTGAATCAGC GTGCATACAA ACTCTCCTGC CTGCTCCTCC TGGGCCCCAG CCCCAGCCCC	180
ATCACAGCTC ACTGCTCTGT TCATCCAGGC CCAGCATGTA GTGGCTGATT CTTCTTGGCT	240
GCTTTTAGCC TCCANAAGTT TCTCTGAAGC CAACCAAACC TCTANGTGTAGGCATGCTG	300
GCCCTGGT	308

## (2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 295 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

ACCTTGCTCG GTGCTTGGAA CATATTAGGA ACTCAAATA TGAGATGATA ACAGTGCCTA	60
TTATTGATTA CTGAGAGAAC TGTAGACAT TTAGTTGAAG ATTTTCTACA CAGGAACGTGA	120
GAATAGGAGA TTATGTTGG CCCTCATATT CTCTCCTATC CTCCCTTGCT CATTCTATGT	180
CTAATATATT CTCATCAAA TAAGGTTAGC ATAATCAGGA AATCGACCAA ATACCAATAT	240
AAAACCAGAT GTCTATCCTT AAGATTTCA AATAGAAAAC AAATTAACAG ACTAT	295

## (2) INFORMATION FOR SEQ ID NO:157:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 126 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

ACAAGTTAA ATAGTGTGT CACTGTGCAT GTGCTGAAAT GTGAAATCCA CCACATTCT	60
GAAGAGCAAA ACAAAATTCTG TCATGTAATC TCTATCTTGG GTCTGGGTA TATCTGTCCC	120
CTTAGT	126

## (2) INFORMATION FOR SEQ ID NO:158:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 442 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

ACCCACTGGT CTTGGAAACA CCCATCCTTA ATACGATGAT TTTTCTGTCG TGTGAAAATG	60
AANCCAGCAG GCTGCCCTA GTCAGTCCTT CCTTCCAGAG AAAAAGAGAT TTGAGAAAGT	120
GCCTGGGTAA TTCACCATT AATTCCCTCC CCAAACCTCTC TGAGTCTTCC CTTAATATT	180
CTGGTGGTTC TGACCAAAGC AGGTCACTGGT TTGTTGAGCA TTTGGGATCC CAGTGAAGTA	240
NATGTTGTA GCCTTGATA CTTAGCCCTT CCCACGCACA AACGGAGTGG CAGAGTGGT	300
CCAACCCCTGT TTICCCAGTC CACGTAGACA GATTCACAGT GCGGAATTCT GGAAGCTGGA	360
NACAGACGGG CTCTTTGCAAG AGCCGGGACT CTGAGANGGA CATGAGGGCC TCTGCCTCTG	420
TGTTCAATTCT CTGATGTCT GT	442

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

ACTTCCAGGT AACGTTGTTG TTTCCGTTGA GCCTGAAC TG ATGGGTGACG TTGTAGGTT	60
TCCAACAAGA ACTGAGGTTG CAGAGCAGGT AGGGAAAGAGT GCTGTTCCAG TTGCACCTGG	120
GCTGCTGTGG ACTGTTGTTG ATTCCCTCACT ACGGCCAAG GTTGTGGAAC TGGCANAAAG	180
GTGTGTTGTT GGANTTGAGC TCGGGCGGCT GTGGTAGGTT GTGGGCTCTT CAACAGGGGC	240
TGCTGTGGTG CCGGGANGTG AANGTGTGTT GTCACTTGAG CTTGGCCAGC TCTGGAAGT	300
ANTANATTCT TCCTGAAGGC CAGCGCTTGT GGAGCTGGCA NGGGTCANTG TTGTGTGTA	360
CGAACCCAGTG CTGCTGTGGG TGGGTGTANA TCCTCCACAA AGCCTGAAGT TATGGTGT	420
TCAGGTAANA ATGTGGTTTC AGTGTCCCTG GGCNGCTGTG GAAGGTTGTA NATTGTCA	480
AAGGAAATAA GCTGTGGT	498

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

ACCTGCATCC AGCTTCCCTG CCAAACATCAC AAGGAGACAT CAACCTCTAG ACAGGGAAAC	60
AGCTTCAGGA TACTTCCAGG AGACAGAGCC ACCAGCAGCA AAACAAATAT TCCCATGCCT	120
GGAGCATGGC ATAGAGGAAG CTGANAAATG TGGGGTCTGA GGAAGCCATT TGAGTCTGGC	180
CACTAGACAT CTCATCAGCC ACTTGTGTGA AGAGATGCC CATGACCCCA GATGCCTCTC	240
CCACCCCTAC CTCCATCTCA CACACTTGAG CTTTCCACTC TGTATAATTG TAACATCCTG	300
GAGAAAAATG GCAGTTGAC CGAACCTGTT CACAACGGTA GAGGCTGATT TCTAACGAAA	360
CTTGTAGAAT GAAGCCTGGA	380

## (2) INFORMATION FOR SEQ ID NO:161:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

ACTCCACATC CCCTCTGAGC AGGCGGTTGT CGTTCAAGGT GTATTTGGCC TTGCCTGTCA	60
CACTGTCCAC TGGCCCTTA TCCACTTGGT GCTTAATCCC TCGAAAGAGC ATGT	114

## (2) INFORMATION FOR SEQ ID NO:162:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

ACTTTCTGAA TCGAATCAA TGATACTTAG TGTAGTTTA ATATCCTCAT ATATATCAA	60
GTGTTACTAC TCTGATAATT TTGTAAACCA GGTAACCAGA ACATCCAGTC ATACAGCTT	120
TGGTGATATA TAACTGGCA ATAACCCAGT CTGGTGATAC ATAAAACATAC TCACTGT	177

## (2) INFORMATION FOR SEQ ID NO:163:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

CATTTATACA GACAGGGCGTG AAGACATTCA CGACAAAAAC GCGAAATTCT ATCCCGTGAC	60
CANAGAAGGC AGCTACGGCT ACTCCTACAT CCTGGCGTGG GTGGCCTTCG CCTGCACCTT	120
CATCAGCGGC ATGATGT	137

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

CTTATCACAA TGAATGTTCT CCTGGGCAGC GTTGTGATCT TTGCCACCTT CGTGACTTTA	60
TGCAATGCAT CATGCTATTT CATACTTAAT GAGGGAGTTC CAGGAGATTG AACCAAGGAAA	120
TGCATGGATC TCAAAGGAAA CAAACACCCA ATAAACTCGG AGTGGCAGAC TGACAACTGT	180
GAGACATGCA CTTGCTACGA AACAGAAAATT TCATGTTGCA CCCTTGTTTC TACACCTGTG	240
GGTTATGACA AAGACAACGT CCAAAGAATC TTCAAGAAGG AGGACTGCAA GTATATCGTG	300
GTGGAGAAGA AGGACCCAAA AAAGACCTGT TCTGTCAGTG AATGGATAAT CTAATGTGCT	360
TCTAGTAGGC ACAGGGCTCC CAGGCCAGGC CTCATTCTCC TCTGGCCTCT AATAGTCAAT	420
GATTGTGTAG CCATGCCTAT CAGTAAAAAG ATNTTTGAGC AAACACTTT	469

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

ACAGTTTTTT ATANATATCG ACATTGCCGG CACTTGTGTT CAGTTTCATA AAGCTGGTGG	60
ATCCGCTGTC ATCCACTATT CCTTGGCTAG AGTAAAATT ATTCTTATAG CCCATGTCCC	120
TGCAGGCCGC CCGCCCGTAG TTCTCGTTCC AGTCGTCTTG GCACACAGGG TGCCAGGACT	180
TCCTCTGAGA TGAGT	195

## (2) INFORMATION FOR SEQ ID NO:166:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 383 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

ACATCTTAGT AGTGTGGCAC ATCAGGGGGC CATCAGGGTC ACAGTCACTC ATAGCCTCGC	60
CGAGGTCGGA GTCCACACCA CCGGTGTAAG TGTGCTCAAT CTTGGGCTTG GCGCCCACCT	120
TTGGAGAAGG GATATGCTGC ACACACATGT CCACAAAGCC TGTGAACCTCG CCAAAGAATT	180
TTTGCAGACC AGCCTGAGCA AGGGGCGGAT GTTCAGCTTC AGCTCCTCCT TCGTCAGGTG	240
GATGCCAACC TCGTCTANGG TCCGTGGGAA GCTGGTGTCC ACNTCACCTA CAAACCTGGGC	300
GANGATCTTA TAAAGAGGCT CCNAGATAAA CTCCACGAAA CTTCTCTGGG AGCTGCTAGT	360
NGGGGCCTTT TTGGTGAAC TTC	383

## (2) INFORMATION FOR SEQ ID NO:167:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 247 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

ACAGAGCCAG ACCTTGGCCA TAAATGAANC AGAGATTAAG ACTAAACCCC AAGTCGANAT	60
TGGAGCAGAA ACTGGAGCAA GAAGTGGGCC TGGGGCTGAA GTAGAGACCA AGGCCACTGC	120
TATANCCATA CACAGAGCCA ACTCTCAGGC CAAGGCNATG GTTGGGGCAG ANCCAGAGAC	180
TCAATCTGAN TCCAAAGTGG TGGCTGGAAC ACTGGTCATG ACANAGGCAG TGACTCTGAC	240
TGANGTC	247

## (2) INFORMATION FOR SEQ ID NO:168:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 273 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

ACTTCTAAGT TTTCTAGAAG TGGAAGGATT GTANTCATCC TGAAAATGGG TTTACTTCAA	60
AATCCCTCAN CCTTGTCTT CACNACTGTC TATACTGANA GTGTCATGTT TCCACAAAGG	120
GCTGACACCT GAGCCTGNAT TTTCACTCAT CCCTGAGAAG CCCTTCCAG TAGGGTGGGC	180
AATTCCCAAC TTCCTTGCCA CAAGCTTCCC AGGCTTCTC CCCTGGAAA CTCCAGCTTG	240
AGTCCCAGAT ACACTCATGG GCTGCCCTGG GCA	273

## (2) INFORMATION FOR SEQ ID NO:169:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

ACAGCCTTGG CTTCCCCAAA CTCCACAGTC TCAGTGCAGA AAGATCATCT TCCAGCAGTC	60
AGCTCAGACC AGGGTCAAAG GATGTGACAT CAACAGTTTC TGGTTTCAGA ACAGGTTCTA	120
CTACTGTCAA ATGACCCCCC ATACTTCCTC AAAGGCTGTG GTAAGTTTG CACAGGTGAG	180
GGCAGCAGAA AGGGGTANT TACTGATGGA CACCATCTTC TCTGTATACT CCACACTGAC	240
CTTGCCATGG GCAAAGGCC CTACCACAAA ACAATAGGA TCACTGCTGG GCACCAGCTC	300
ACGCACATCA CTGACAACCG GGATGGAAA AGAANTGCCA ACTTTCATAC ATCCAACCTGG	360
AAAGTGATCT GATACTGGAT TCTTAATTAC CTTCAAAGC TTCTGGGGC CATCAGCTGC	420
TCGAACACTG A	431

## (2) INFORMATION FOR SEQ ID NO:170:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

ACCTGTGGGC TGGGCTGTTA TGCTGTGCC GGCTGCTGAA AGGGAGTTCA GAGGTGGAGC	60
TCAAGGAGCT CTGCAGGCAT TTTGCCAANC CTCTCCANAG CANAGGGAGC AACCTACACT	120
CCCCGCTAGA AAGACACCAAG ATTGGAGTCC TGGGAGGGGG AGTTGGGTG GGCATTTGAT	180
GTATACTTGT CACCTGAATG AANGAGCCAG AGAGGAANGA GACCAANATG ANATTGGCCT	240
TCAAAGCTAG GGGTCTGGCA GGTGGA	266

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

GGCAGCCAAA	TCATAAACGG	CGAGGACTGC	AGCCGCACT	CGCAGCCCTG	GCAGGGCGCA	60
CTGGTCATGG	AAAACGAATT	GTTCGCTCG	GGCGCTCTGG	TGCATCCGCA	GTGGGTGCTG	120
TCAGCCGCAC	ACTGTTTCCA	GAAGTGAGTG	CAGAGCTCCT	ACACCATCGG	GCTGGGCCTG	180
CACAGTCTTG	AGGGCGACCA	AGAGCCAGGG	AGCCAGATGG	TGGAGGCCAG	CCTCTCCGTA	240
CGGCACCCAG	AGTACAACAG	ACCCCTGCTC	GCTAACGACC	TCATGCTCAT	CAAGTTGGAC	300
GAATCCGTGT	CCGAGTCTGA	CACCATCCGG	AGCATCAGCA	TTGCTTCGCA	GTGCCCTACC	360
GCGGGGAACT	CTTGCCCTCGT	TTCTGGCTGG	GGTCTGCTGG	CGAACGGCAG	AATGCCTACC	420
GTGCTGCAGT	GCGTGAACGT	GTGGTGGTG	TCTGAGGAGG	TCTGAGTAA	GCTCTATGAC	480
CCGCTGTACC	ACCCCAGCAT	GTTCGCGCC	GGCGGAGGGC	AAGACCAAGAA	GGACTCCTGC	540
AACGGTGACT	CTGGGGGGCC	CCTGATCTGC	AACGGGTACT	TGCAGGGCCT	TGTGCTTTG	600
GGAAAAGCCC	CGTGTGGCCA	AGTTGGCTG	CCAGGGTGTCT	ACACCAACCT	CTGCAAATTG	660
ACTGAGTGGA	TAGAGAAAAC	CGTCCAGGCC	AGTTAACTCT	GGGGACTGGG	AACCCATGAA	720
ATTGACCCCC	AAATACATCC	TGCGGAAGGA	ATTCAAGGAAT	ATCTGTTCCC	AGCCCCCTCCT	780
CCCTCAGGCC	CAGGAGTCCA	GGCCCCCAGC	CCCTCCTCCC	TCAAACCAAG	GGTACAGATC	840
CCCAGCCCC	CCTCCCTCAG	ACCCAGGAGT	CCAGACCCCC	CAGCCCCCTCC	TCCCTCAGAC	900
CCAGGAGTCC	AGCCCCCTCC	CCCTCAGACC	CAGGAGTCCA	GACCCCCCAG	CCCTCCTCC	960
CTCAGACCCA	GGGGTCCAGG	CCCCCAACCC	CTCCCTCCCTC	AGACTCAGAG	GTCCAAGGCC	1020
CCAACCCNTC	ATTCCCCAGA	CCCAGAGGTC	CAGGTCCCAG	CCCTCCTCC	CTCAGACCCA	1080
GCGGTCCAAT	GCCACCTAGA	CTNTCCCTGT	ACACAGTGCC	CCCTTGTGGC	ACGTTGACCC	1140
AACCTTACCA	GTTGGTTTTT	CATTTTTNGT	CCCTTCCCGG	TAGATCCAGA	AATAAAGTTT	1200
AAGAGAAGNG	CAAAAAAAA	AAAAAAA	AAAAAAA	AAAAAAA	AAAAAAA	1248

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Met Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro  
1 5 10 15

Leu Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser  
 20 25 30

Glu Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr  
 35 40 45

Ala Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly  
 50 55 60

Arg Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu  
 65 70 75 80

Glu Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe  
 85 90 95

Cys Ala Gly Gly Gln Xaa Gln Xaa Asp Ser Cys Asn Gly Asp Ser  
 100 105 110

Gly Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe  
 115 120 125

Gly Lys Ala Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn  
 130 135 140

Leu Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser  
 145 150 155

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

GGCAGCCCGC	ACTCGCAGCC	CTGGCAGCG	GCACGGTCA	TGGAAAACGA	ATTGTTCTGC	60
TCGGGCGTCC	TGGTGCATCC	GCAGTGGGTG	CTGTCAGCCG	CACACTGTT	CCAGAACTCC	120
TACACCATCG	GGCTGGGCCT	GCACAGTCTT	GAGGCCGACC	AAGAGCCAGG	GAGCCAGATG	180
GTGGAGGCCA	GCCTCTCCGT	ACGGCACCCA	GAGTACAACA	GACCCCTTGCT	CGCTAACGAC	240
CTCATGCTCA	TCAAGTTGGA	CGAATCCGTG	TCCGAGTCTG	ACACCATCCG	GAGCATCAGC	300
ATTGCTTCGC	AGTGCCTAC	CGCGGGGAAC	TCTTGCTCG	TTTCTGGCTG	GGGTCTGCTG	360
GCGAACGGTG	AGCTCACGGG	TGTGTGTCTG	CCCTCTTCAA	GGAGGTCCCTC	TGCCCAGTCG	420
CGGGGGCTGA	CCCAAGAGCTC	TGCGTCCCAG	GCAGAATGCC	TACCGTGCTG	CAGTGCCTGA	480
ACGTGTCGGT	GGTGTCTGAG	GAGGTCTGCA	GTAAGCTCTA	TGACCCGCTG	TACCACCCCA	540
GCATGTTCTG	CGCCGGCGGA	GGGCAAGACC	AGAAGGACTC	CTGCAACGGT	GACTCTGGGG	600
GGCCCCTGAT	CTGCAACGGG	TACTTGCAGG	GCCTTGTGTC	TTTCGGAAAA	GCCCCGTGTG	660
GCCAAGTTGG	CGTGCCAGGT	GTCTACACCA	ACCTCTGCAA	ATTCACTGAG	TGGATAGAGA	720

AAACCGTCCA GGCCAGTTAA CTCTGGGAC TGGGAACCCA TGAAATTGAC CCCCAAATAC	780
ATCCTGCGGA AGGAATTCAAG GAATATCTGT TCCCAGCCCC TCCCTCCCTCA GGCCCAGGAG	840
TCCAGGCCCC CAGCCCCCTCC TCCCTCAAAC CAAGGGTACA GATCCCCAGC CCCTCCTCCC	900
TCAGACCCAG GAGTCCAGAC CCCCCAGCCC CTCCCTCCCTC AGACCCAGGA GTCCAGCCCC	960
TCCTCCNTCA GACCCAGGAG TCCAGACCCC CCAGCCCCCTC CTCCCTCAGA CCCAGGGTT	1020
GAGGCCCCCA ACCCCCTCCTC CTTCAGAGTC AGAGGTCCAA GCCCCCAACC CCTCGTTCCC	1080
CAGACCCAGA GGTNNAGGTG CCAGCCCCCTC TTCCNTCAGA CCCAGNGGTC CAATGCCACC	1140
TAGATTTTCC CTGNACACAG TGCCCCCTTG TGGNANGTTG ACCAACCTT ACCAGTTGGT	1200
TTTCATTTT TNGTCCCTTT CCCCTAGATC CAGAAATAAA GTTTAAGAGA NGNGCAAAAA	1260
AAAAAA	1265

## (2) INFORMATION FOR SEQ ID NO:174:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

GGTCAGCCGC ACACGTGTTTC CAGAAGTGAG TGCAGAGCTC CTACACCATC GGGCTGGCC	60
TGCACAGTCT TGAGGCCGAC CAAGAGCCAG GGAGCCAGAT GGTGGAGGCC AGCCTCTCCG	120
TACGGCACCC AGAGTACAAC AGACCCCTTGC TCGCTAACGA CCTCATGCTC ATCAAGTTGG	180
ACGAATCCGT GTCCGAGTCT GACACCATCC GGAGCATCAG CATTGCTTCG CAGTGCCTA	240
CCGCGGGGAA CTCTGCCTC GTTTCTGGCT GGGGTCTGCT GGCAGACGGT GAGCTCACGG	300
GTGTGTGTC GGCCTCTTCA AGGAGGTCTT CTGCCAGTC GCGGGGGCTG ACCCAGAGCT	360
CTGCGTCCCA GGCAGAATGC CTACCGTGCT GCAGTGGTGT AACGTGTCGG TGGTGTCTGA	420
NGAGGTCTGC ANTAAGCTCT ATGACCCGCT GTACCACCCCC ANCATGTTCT GCGCCGGCGG	480
AGGGCAAGAC CAGAAGGACT CCTGCAACGT GAGAGAGGGG AAAGGGGAGG GCAGGGGACT	540
CAGGGAAAGGG TGGAGAAGGG GGAGACAGAG ACACACAGGG, CCGCATGGCG AGATGCAGAG	600
ATGGAGAGAC ACACAGGGAG ACAGTGACAA CTAGAGAGAG AAACTGAGAG AAACAGAGAA	660
ATAAACACAG GAATAAAGAG AAGCAAAGGA AGAGAGAAAC AGAAACAGAC ATGGGGAGGC	720
AGAAACACAC ACACATAGAA ATGCAGTTGA CCTTCCAACA GCATGGGGCC TGAGGGCGGT	780
GACCTCCACC CAATAGAAAA TCCCTTATA ACTTTTGACT CCCCCAAAAC CTGACTAGAA	840
ATAGCCTACT GTTGACGGG AGCCTTACCA ATAACATAAA TAGTCGATTT ATGCATACGT	900
TTTATGCATT CATGATATAC CTTTGTGGT ATTTTTGAT ATTCTAAGC TACACAGTTC	960
GTCTGTGAAT TTTTTAAAT TGGTCAACT CTCCTAAAAT TTTCTGATG TGTGTTATTGA	1020
AAAAATCCAA GTATAAGTGG ACTTGTGCAT TCAAACCCAGG GTTGGTCAAG GGTCAACTGT	1080
GTACCCAGAG GGAAACAGTG ACACAGATTG ATAGAGGTGA AACACGAAGA GAAACAGGAA	1140
AAATCAAGAC TCTACAAAAGA GGCTGGCAG GGTGGCTCAT GCCTGTAATC CCAGCACTTT	1200
GGGAGGCGAG GCAGGCAGAT CACTTGAGGT AAGGAGTTCA AGACCAAGCCT GGCCAAAATG	1260
GTGAAATCCT GTCTGTACTA AAAATACAAA AGTTAGCTGG ATATGGTGGC AGGCGCCTGT	1320
AATCCCAGCT ACTTGGGAGG CTGAGGCAGG AGAATTGCTT GAATATGGGA GGCAGAGGTT	1380
GAAGTGAGTT GAGATCACAC CACTATACTC CAGCTGGGC AACAGAGTAA GACTCTGTCT	1440
CAAAAAAAAAA AAAAAAAAAA	1459

## (2) INFORMATION FOR SEQ ID NO:175:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1167 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

GC	GCAGCCCT	GGCAGGGGGC	ACTGGTCATG	AAAAACGAAT	TGTTCTGCTC	GGCGTCCTG	60
GT	GCATCCGC	AGTGGGTGCT	GTCAGCCGCA	CACTGTTCC	AGAACTCCTA	CACCATCGGG	120
CT	GGGCTGCA	ACAGTCTGA	GGCCGACCAA	GAGCCAGGGA	GCCAGATGGT	GGAGGCCAGC	180
CT	CTCCGTAC	GGCACCCAGA	GTACAACAGA	CTCTTGCTCG	CTAACGACCT	CATGCTCATC	240
AAG	TGGACG	AATCCGTGTC	CGAGTCTGAC	ACCATCCGGA	GCATCAGCAT	TGCTTCGAG	300
TG	CCCTACCG	CGGGGAACTC	TTGCCCTCGTN	TCTGGCTGGG	GTCTGCTGGC	GAACGGCAGA	360
AT	GCCTACCG	TGCTGCACTG	CGTGAACGTG	TCGGTGGTGT	CTGAGGAGNT	CTGCAGTAAG	420
CT	CTATGACC	CGCTGTACCA	CCCCAGCATG	TTCTGCGCCG	GCGGAGGGCA	AGACCAGAAG	480
GACT	CCCTGCA	ACGGTGACTC	TGGGGGGCCC	CTGATCTGCA	ACGGGTACTT	GCAGGGCCTT	540
GT	GTCTTTCG	AAAAAGCCCC	GTGTGGCCAA	CTTGGCGTGC	CAGGTGTCTA	CACCAACCTC	600
TG	CAAATTCA	CTGAGTGGAT	AGAGAAAACC	GTCCAGNCCA	GTAACTCTG	GGGACTGGGA	660
ACCCATGAAA	TTGACCCCCA	AATACATCCT	GCGGAANGAA	TTCAGGAATA	TCTGTTCCA	720	
GCCCCTCCTC	CCTCAGGGCCC	AGGAGTCCAG	GCCCCCAGCC	CCTCCTCCCT	CAAACCAAGG	780	
GTACAGATCC	CCAGCCCCCTC	CTCCCTCAGA	CCCAGGAGTC	CAGACCCCCC	AGCCCCCTCNT	840	
CCNTCAGACC	CAGGAGTCCA	GCCCCCTCCTC	CNTCAGACGC	AGGAGTCCAG	ACCCCCCAGC	900	
CCNTCNTCCG	TCAGACCCAG	GGGTGCAGGC	CCCCAACCCC	TCTTCCNTCA	GAGTCAGAGG	960	
TCCAAGCCCC	CAACCCCTCG	TTCCCCAGAC	CCAGAGGTNC	AGGTCCCAGC	CCCTCCTCCC	1020	
TCAGACCCAG	CGGTCCAATG	CCACCTAGAN	TNTCCCTGTA	CACAGTGCC	CCTTGTGGCA	1080	
NGTTGACCCA	ACCTTACCAAG	TTGGTTTTTC	ATTTTTGTC	CCTTCCCCT	AGATCCAGAA	1140	
ATAAAGTNTA	AGAGAAGCGC	AAAAAAA				1167	

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Met	Glu	Asn	Glu	Leu	Phe	Cys	Ser	Gly	Val	Leu	Val	His	Pro	Gln	Trp
1				5					10			15			

Val	Leu	Ser	Ala	Ala	His	Cys	Phe	Gln	Asn	Ser	Tyr	Thr	Ile	Gly	Leu
20							25					30			

Gly	Leu	His	Ser	Leu	Glu	Ala	Asp	Gln	Glu	Pro	Gly	Ser	Gln	Met	Val
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35

40

45

Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Leu Leu Leu  
 50 55 60

Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser  
 65 70 75 80

Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly  
 85 90 95

Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg Met  
 100 105 110

Pro Thr Val Leu His Cys Val Asn Val Ser Val Val Ser Glu Xaa Val  
 115 120 125

Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys Ala  
 130 135 140

Gly Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly  
 145 150 155 160

Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly Lys  
 165 170 175

Ala Pro Cys Gly Gln Leu Gly Val Pro Gly Val Tyr Thr Asn Leu Cys  
 180 185 190

Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Xaa Ser  
 195 200 205

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1119 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

GCGCACTCGC	AGCCCTGGCA	GGCGGCAGTG	GTCATGGAAA	ACGAATTGTT	CTGCTCGGGC	60
GTCCTGGTGC	ATCCGCAGTG	GGTGCTGTCA	GCCGCACACT	GTTCCAGAA	CTCCTACACC	120
ATCGGGCTGG	GCCTGCACAG	TCTTGAGGCC	GA <sup>CA</sup> AGAGC	CAGGGAGCCA	GATGGTGGAG	180
GCGAGCCTCT	CCGTACGGCA	CCCAGAGTAC	AACAGACCCT	TGCTCGCTAA	CGACCTCATG	240
CTCATCAAGT	TGGACGAATC	CGTGTCCGAG	TCTGACACCA	TCCGGAGCAT	CAGCATTGCT	300
TCGCAGTGCC	CTACCGCGGG	GAACCTCTGC	CTCGTTCTG	GCTGGGGTCT	GCTGGCGAAC	360
GATGCTGTGA	TTGCCATCCA	GTCCCAGACT	GTGGGAGGCT	GGGAGTGTGA	GAAGCTTCC	420
CAACCCTGGC	AGGGTTGTAC	CATTCGGCA	ACTTCCAGTG	CAAGGACGTC	CTGCTGCATC	480

CTCACTGGGT GCTCACTACT GCTCACTGCA TCACCCGGAA CACTGTGATC AACTAGCCAG	540
CACCATAGTT CTCCGAAGTC AGACTATCAT GATTACTGTG TTGACTGTGC TGTCTATTGT	600
ACTAACCATG CCGATGTTA GGTAAATTG GCGTCACITG GCCTCAACCA TCTTGGTATC	660
CAGTTATCCT CACTGAATTG AGATTTCCCTG CTTCAAGGTGTC AGCCATTCCC ACATAATTTC	720
TGACCTACAG AGGTGAGGGG TCATATAGCT CTTCAAGGAT GCTGGTACTC CCCTCACAAA	780
TTCATTTCTC CTGTTGTAGT GAAAGGTGCG CCCTCTGGAG CCTCCAGGG TGGGTGTGCA	840
GGTCACAATG ATGAATGTAT GATCGTGTTC CCATTACCCA AAGCCTTTAA ATCCCTCATG	900
CTCAGTACAC CAGGGCAGGT CTAGCATTTC TTCATTTAGT GTATGCTGTGCA CATTGCA	960
ACCACCTCAG GACTCCTGGA TTCTCTGCCT AGTTGAGCTC CTGCATGCTG CCTCCTGGG	1020
GAGGTGAGGG AGAGGGCCA TGGTTCAATG GGATCTGTGC AGTTGTAACA CATTAGGTGC	1080
TTAATAAACAA GAAGCTGTGA TGTAAAAAAA AAAAAAAA	1119

## (2) INFORMATION FOR SEQ ID NO:178:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 164 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

Met	Glu	Asn	Glu	Leu	Phe	Cys	Ser	Gly	Val	Leu	Val	His	Pro	Gln	Trp
1				5						10					15

Val	Leu	Ser	Ala	Ala	His	Cys	Phe	Gln	Asn	Ser	Tyr	Thr	Ile	Gly	Leu
				20					25						30

Gly	Leu	His	Ser	Leu	Glu	Ala	Asp	Gln	Glu	Pro	Gly	Ser	Gln	Met	Val
				35				40				45			

Glu	Ala	Ser	Leu	Ser	Val	Arg	His	Pro	Glu	Tyr	Asn	Arg	Pro	Leu	Leu
				50				55			60				

Ala	Asn	Asp	Leu	Met	Leu	Ile	Lys	Leu	Asp	Glu	Ser	Val	Ser	Glu	Ser
	65				70				75						80

Asp	Thr	Ile	Arg	Ser	Ile	Ser	Ile	Ala	Ser	Gln	Cys	Pro	Thr	Ala	Gly
	85								90						95

Asn	Ser	Cys	Leu	Val	Ser	Gly	Trp	Gly	Leu	Leu	Ala	Asn	Asp	Ala	Val
				100					105						110

Ile	Ala	Ile	Gln	Ser	Xaa	Thr	Val	Gly	Gly	Trp	Glu	Cys	Glu	Lys	Leu
		115						120				125			

Ser	Gln	Pro	Trp	Gln	Gly	Cys	Thr	Ile	Ser	Ala	Thr	Ser	Ser	Ala	Arg
				130				135				140			

Thr	Ser	Cys	Cys	Ile	Leu	Thr	Gly	Cys	Ser	Leu	Leu	Leu	Thr	Ala	Ser
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145

150

155

160

Pro Gly Thr Leu

## (2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

CTGGAGTGCCTTGC TTGGTGTTC AAGCCCCTGC AGGAAGCAGA ATGCACCTTC TGAGGCACCT	60
CCAGCTGCC CCGGCCGGGG GATGCGAGGC TCGGAGCACC CTTGCCCGGC TGTGATTGCT	120
GCCAGGCACT GTTCATCTCA GCTTTCTGT CCCTTGCTC CCGGCAAGCG CTTCTGCTGA	180
AAGTTCATAT CTGGAGCCTG ATGTCTTAAC GAATAAGGT CCCATGCTCC ACCCGAAAAA	240
AAAAAAAAAA	250

## (2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

ACTAGTCCAG TGTGGTGGAA TTCCATTGTG TTGGGCCAA CACAATGGCT ACCTTTAACAA	60
TCACCCAGAC CCCGCCCTG CCCGTGCCCC ACGCTGCTGC TAACGACAGT ATGATGCTTA	120
CTCTGCTACT CGGAAACTAT TTTTATGTAA TTAATGTATG CTTTCTGTT TATAAATGCC	180
TGATTTAAAA AAAAAAAAAA AA	202

## (2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 558 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

TCCYTTTGKT NAGGTTTKKG AGACAMCCCK AGACCTWAAN CTGTGTCACA GACTTCYNGG	60
AATGTTAGG CAGTGTAGT AATTCYTCG TAAATGATTCT GTTATTACTT TCCTNATTCT	120
TTATTCCTCT TTCTCTGAA GATTAATGAA GTTGAAAATT GAGGTGGATA AATACAAAAA	180
GGTAGTGTGA TAGTATAAGT ATCTAAGTGC AGATGAAAGT GTGTTATATA TATCCATTCA	240
AAATTATGCA AGTTAGTAAT TACTCAGGGT TAACTAAATT ACTTTAATAT GCTGTTGAAC	300
CTACTCTGTT CCTTGCTAG AAAAAATTAA AACAGGACT TTGTTAGTTT GGGAAAGCCAA	360
ATTGATAATA TTCTATGTTA TAAAAGTTGG GCTATACATA AATTATTAAG AAATATGGAW	420

TTTTATTCCC AGGAATATGG KGTTCATTT ATGAATATTA CSCRGGATAG AWGTWTGAGT	480
AAAAYCAGTT TTGGTWAATA YGTWAATATG TCMTAAATAA ACAAKGCTTT GACTTATTC	540
CAAAAAAAA AAAAAAAA	558

## (2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

ACAGGGWTTK GRGGATGCTA AGSCCCRG A RWTYGTGTTGA TCCAACCCTG GCTTWTGTTTC	60
AGAGGGAAA ATGGGGCTA GAAGTTACAG MSCATYTAGY TGGTGCGMTG GCACCCCTGG	120
CSTCACACAG ASTCCCGAGT AGCTGGGACT ACAGGCACAC AGTCACTGAA GCAGGCCCTG	180
TTWGCAATT C ACGTTGCCAC CTCCAACCTTA AACATTCTTC ATATGTGATG TCCTTAGTCA	240
CTAAGGTTAA ACTTTCCCAC CCAGAAAAGG CAACTTAGAT AAAATCTTAG AGTACTTTCA	300
TACTMTTCTA AGTCCTCTTC CAGCCTCACT KKGAGTCCTM CYTGGGGGTT GATAGGAANT	360
NTCTCTTGGC TTTCTCAATA AARTCTCTAT YCATCTCATG TTTAATTG TACGCATARA	420
AWTGSTGARA AAATTAAAAT GTTCTGGTTY MACTTTAAAA ARAAAAAAAA AAAAAAAA	479

## (2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

AGGCAGGGAGC AGAAGCTAAA GCCAAAGCCC AAGAAGAGTG GCAGTGCCAG CACTGGTGCC	60
AGTACCAAGTA CCAATAACAG TGCCAGTGCC AGTGCAGCA CCAGTGGTGG CTTCAGTGCT	120
GGTGCAGCC TGACCGCCAC TCTCACATTG GGGCTCTTCG CTGGCCTTGG TGGAGCTGGT	180
GCCAGCACCA GTGGCAGCTC TGGTGCCTGT GGTTTCTCCT ACAAGTGAGA TTTTAGATAT	240
TGTTAACCTT GCCAGTCTTT CTCTTCAGC CAGGGTGCAT CCTCAGAAAC CTACTCAACA	300
CAGCACTCTA GGCAGCCACT ATCAATCAAT TGAAGTTGAC ACTCTGCATT ARATCTATTT	360
GCCATTCAA AAAAAAAA AAAA	384

## (2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

ACCGAATTGG GACCGCTGGC TTATAAGCGA TCATGTYYNT CCRGTATKAC CTCAACGAGC	60
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AGGGAGATCG AGTCTATAACG CTGAAGAAAT TTGACCCGAT GGGACAACAG ACCTGCTCAG	120
CCCATCCTGC TCGGTTCTCC CCAGATGACA AATACTCTSG ACACCGAATC ACCATCAAGA	180
AACGCTTCAA GGTGCTCATG ACCCAGCAAC CGCGCCCTGT CCTCTGAGGG TCCCTTAAAC	240
TGATGCTTT TCTGCCACCT GTTACCCCTC GGAGACTCCG TAACCAAAC TTTGGACTG	300
TGAGCCCTGA TGCCCTTTTG CCAGCCATAC TCTTGGCAT CCAGTCTCTC GTGGCGATTG	360
ATTATGCTTG TGTGAGGCAA TCATGGTGGC ATCACCCATA AAGGAAACAC ATTTGACTTT	420
TTTTCTCAT ATTTAAATT ACTACMAGAW TATTWMAGAW WAAATGAWTG GAAAAACTST	480
TAAAAAAA AAAAAA	496

## (2). INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

GCTGGTAGCC TATGGCGKGG CCCACGGAGG GGCTCCTGAG GCCACGGRAC AGTGACTTCC	60
CAAGTATCYT GCGCGCGTC TTCTACCGTC CCTACCTGCA GATCTTCGGG CAGATTCCCC	120
AGGAGGACAT GGACGTGGCC CTCATGGAGC ACAGCAACTG YTCGTCGGAG CCCGGCTTCT	180
GGGCACACCC TCCTGGGGCC CAGGCGGGCA CCTGCGTCTC CCAGTATGCC AACTGGCTGG	240
TGGTGCTGCT CCTCGTCATC TTCCCTGCTCG TGGCAACAT CCTGCTGGTC AACTTGCTCA	300
TTGCCATGTT CAGTTACACA TTGGCAAAAG TACAGGGCAA CAGCGATCTC TACTGGGAAG	360
GCGCAGCGTT ACCGCCTCAT CCGG	384

## (2). INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 577 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

GAGTTAGCTC CTCCACAAACC TTGATGAGGT CGTCTGCAGT GGCCCTCTCGC TTCATACCGC	60
TNCCATCGTC ATACTGTAGG TTTGCCACCA CYTCCTGGCA TCTTGGGGCG GCNTAAATT	120
CCAGGAAACT CTCAATCAAG TCACCGTCGA TGAAACCTGT GGGCTGGTTC TGTCTCCGC	180
TCGGTGTGAA AGGATCTCCC AGAAGGAGTG CTCGATCTTC CCCACACTTT TGATGACTTT	240
ATTGAGTCGA TTCTGCATGT CCAGCAGGAG GTTGTACAG CTCTCTGACA GTGAGGTAC	300
CAGCCCTATC ATGCCGTTGA MCGTGCCGAA GARCACCGAG CCTTGTGTGG GGGKKGAAGT	360
CTCACCCAGA TTCTGCATTA CCAGAGAGCC GTGGCAAAAG ACATTGACAA ACTCGCCAG	420
GTGGAAAAG AMCAMCTCCT GGARGTGCTN GCCGCTCCTC GTCMGTGTTGGT GGCAGCGCTW	480
TCCTTTGAC ACACAAACAA GTTAAAGGCA TTTTCAGCCC CCAGAAANTT GTCATCATCC	540
AAGATNTCGC ACAGCACTNA TCCAGTTGGG ATTAAT	577

## (2). INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

AACATCTTCC	TGTATAATGC	TGTGTAATAT	CGATCCGATN	TTGTCTGSTG	AGAATYCATW	60
ACTKGGAAAA	GMAACATTAA	AGCCTGGACA	CTGGTATTAA	AATTACAAT	ATGCAACACT	120
TTAACACAGTG	TGTCAATCTG	CTCCCYYNAC	TTTGTCATCA	CCAGTCTGGG	AAKAAGGGTA	180
TGCCCTATTG	ACACCTGTTA	AAAGGGCGCT	AAGCATTTTT	GATTCAACAT	CTTTTTTTT	240
GACACAAGTC	CGAAAAAAAGC	AAAAGTAAAC	AGTTATYYAT	TTGTTAGCCA	ATTCACTTTC	300
TTCATGGGAC	AGAGCCATYT	GATTTAAAAA	GCAAATTGCA	TAATATTGAG	CTTYGGGAGC	360
TGATATTTGA	GCGGAAGAGT	AGCCTTTCTA	CTTCACCAGA	CACAACCTCCC	TTTCATATTG	420
GGATGTTNAC	NAAAGTWATG	TCTCTWACAG	ATGGGATGCT	TTTGTGGCAA	TTCTGTTCTG	480
AGGATCTCCC	AGTTTATTAA	CCACTTGCAC	AAGAAGGCCT	TTTCTTCCTC	AGGC	534

(2) INFORMATION FOR SEQ ID NO:188:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 761 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

AGAAACCAGT	ATCTCTNAAA	ACAACCTCTC	ATACCTTGTG	GACCTAATTT	TGTGTGCGTG	60
TGTGTGTGCG	CGCATATTAT	ATAGACAGGC	ACATCTTTT	TACTTTGTG	AAAGCTTATG	120
CCTCTTGGT	ATCTATATCT	GTGAAAGTTT	TAATGATCTG	CCATAATGTC	TTGGGGACCT	180
TTGTCTTCTG	TGTAAATGGT	ACTAGAGAAA	ACACCTATNT	TATGAGTC	TCTAGTTNGT	240
TTTATTGAC	ATGAAGGAAA	TTTCCAGATN	ACAACACTNA	CAAACACTCC	CTKGACKARG	300
GGGGACAAAG	AAAAGCAAAA	CTGAMCATAA	RAAACAAATWA	CCTGGTGAGA	ARTTGCATAA	360
ACAGAAATWR	GGTAGTATAT	TGAARNACAG	CATCATTAAA	RMGTTWTKTT	WTTCCTCCTT	420
GCAAAAAACA	TGTACNGACT	TCCCCTTGAG	TAATGCCAAG	TTGTTTTTTT	TATNATAAAA	480
CTTGCCCTTC	ATTACATGTT	TNAAAGTGGT	GTGGTGGGCC	AAAATATTGA	AATGATGGAA	540
CTGACTGATA	AAGCTGTACA	AATAAGCAGT	GTGCCCTAAC	AGCAACACAG	TAATGTTGAC	600
ATGCTTAATT	CACAAATGCT	AATTCATTA	AAATGTTTG	CTAAATACA	CTTTGAAC	660
TTTTTCTGTN	TTCCCAGAGC	TGAGATNTT	GATTTTATGT	AGTATNAAGT	AAAAANTAC	720
GAAAATAATA	ACATTGAAGA	AAAANANAAA	AAANAAAAAA			761

(2) INFORMATION FOR SEQ ID NO:189:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

TTTTTTTTTT	TTTGCCTGATN	CTACTATTTT	ATTGCAGGAN	GTGGGGGTGT	ATGCACCGCA	60
CACCGGGGCT	ATNAGAAGCA	AGAAGGAAGG	AGGGAGGGCA	CAGCCCCTTG	CTGAGCAACA	120
AAGCCGCGCTG	CTGCCTCTC	TGTCTGTCTC	CTGGTGCAGG	CACATGGGGA	GACCTTCCCC	180

AAGGCAGGGG	CCACCAGTCC	AGGGGTGGGA	ATACAGGGGG	TGGGANGTGT	GCATAAGAAG	240
TGATAGGCAC	AGGCCACCCG	GTACAGACCC	CTCGGCTCCT	GACAGGTNGA	TTTCGACCAG	300
GTCATTGTGC	CCTGCCAGG	CACAGCGTAN	ATCTGGAAAA	GACAGAAATGC	TTTCCTTTTC	360
AAATTTGGCT	NGTCATNGAA	NGGGCANITT	TCCAANTTNG	GCTNGGTCTT	GGTACNCCTTG	420
GTTCGGGCCA	GCTCCNCGTC	CAAAAANTAT	TCACCCNNCT	CCNAATTGCT	TGCNGGNCCC	480
CC						482

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

TTTTTTTTTT	TTTAAACACA	GTCCCCACACA	ACAAAATTTA	TTAGAAGAAT	AGTGGTTTG	60
AAAACCTCTG	CATCCAGTGA	GAACCTACCAT	ACACCACATT	ACAGCTNGGA	ATGTNCTCCA	120
AATGTCTGGT	CAAATGATAC	AATGGAAACCA	TTCAATCTTA	CACATGCACG	AAAGAACAAAG	180
CGCTTTGAC	ATACAATGCA	CAAAAAAAAG	AGGGGGGGGG	GACCACATGG	ATTAAAATTT	240
TAAGTACTCA	TCACATACAT	TAAGACACAG	TTCTAGTCCA	GTCNAAAATC	AGAACTGCNT	300
TGAAAAAATT	CATGTATGCA	ATCCAACCAA	AGAACTTNAT	TGGTGTATCAT	GANTNCTCTA	360
CTACATCNAC	CTTGATCATT	GCCAGGAACN	AAAAGTTNAA	ANCACNCNGT	ACAAAAANAA	420
TCTGTAATTN	ANTTCAACCT	CCGTACNGAA	AAATNTNNNT	TATACACTCC	C	471

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

GAGGGATTGA	AGGTCTGTT	C	TASTGTCGGM	CTGTTCA	GCC	ACCAACTCTA	ACAAGTTGCT	60
GTCTTCCACT	CACTGTCTGT		AAGCTTTTA	ACCCAGACWG	TATCTTCATA	AATAGAACAA		120
ATTCTTCACC	AGTCACATCT		TCTAGGACCT	TTTGGATT	AGTTAGTATA	AGCTCTCCA		180
CTTCCTTGT	TAAGACTTCA		TCTGGTAAAG	TCTTAAGTTT	TGTAGAAAGG	AATTYAATTG		240
CTCGTTCTCT	AAACAATGTCC		TCTCCTTGAA	GTATTTGGCT	GAACAACCCA	CCTAAAGTCC		300
CTTTGTGCAT	CCATTTAAA		TATACTTAAT	AGGGCATTGK	TNCACTAGGT	TAAATTCTGC		360
AAGAGTCATC	TGTCTGCAAA		AGTTGCGTTA	GTATATCTGC	CA			402

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

GAGCTCGGAT	CCAATAATCT	TIGTCTGAGG	GCAGCACACA	TATNCAGTGC	CATGGNAACT	60
GGTCTACCCC	ACATGGGAGC	AGCATGCCGT	AGNTATATAA	GGTCATTCCC	TGAGTCAGAC	120
ATGCYTYTTT	GAYTACCGTG	TGCAAGTGC	TGGTGATTCT	YAAACACACYT	CCATCCCGBT	180
CTTTTGTGGA	AAAACCTGGCA	CTTKTCTGGA	ACTAGCARGA	CATCACTTAC	AAATTCAACCC	240
ACGAGACACT	TGAAAGGTGT	AACAAAGCGA	YTCTTGCATT	GCTTTTTGTC	CCTCCGGCAC	300
CAGTTGTCAA	TACTAACCCG	CTGGTTTGCC	TCCATCACAT	TTGTGATCTG	TAGCTCTGGA	360
TACATCTCCT	GACAGTACTG	AAGAACTTCT	TCTTTTGTTT	CAAAGACARC	TCTTGGTGCC	420
TGTTGGATCA	GGTCCCATT	TCCCAGTCYG	AATGTTACACA	TGGCATATT	WACTTCCCAC	480
AAAACATTGC	GATTTGAGGC	TCAGCAACAG	CAAATCCTGT	TCCGGCATTG	GCTGCAAGAG	540
CCTCGATGTA	GCCGGCCAGC	GCCAAGGCAG	GCGCCGTGAG	CCCCACCAGC	AGCAGAAGCA	600
G						601

## (2) INFORMATION FOR SEQ ID NO:193:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 608 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

ATACAGCCCA	NATCCCACCA	CGAAGATCGC	CTTGTGACT	GAGAACCTGA	TGCGGTCACT	60
GGTCCCGCTG	TAGCCCCAGC	GACTCTCCAC	CTGCTGGAAG	CGTTGATGC	TGCACTCYTT	120
CCCAACGCG	GCAGMAGCGG	GSCCGGTCAA	TGAACCTCAY	TCGTGGCTTG	GGGTKGACGG	180
TKAAGTGCAG	GAAGAGGCTG	ACCACCTCGC	GGTCCACCAG	GATGCCCGAC	TGTGCGGGAC	240
CTGCAGCGAA	ACTCCTCGAT	GGTCATGAGC	GGGAAGCGAA	TGAGGCCCAG	GGCCTTGCCC	300
AGAACCTTCC	GCCTGTTCTC	TGGCGTCACC	TGCAGCTGCT	GCCGCTGACA	CTCGGCCTCG	360
GACCAGCGGA	CAAACGGCRT	TGAACAGCCG	CACCTCACCG	ATGCCAGTG	TGTCGCGCTC	420
CAGGAMMGSC	ACCAGCGTGT	CCAGGTCAAT	GTCGGTGAAG	CCCTCCGCGG	GTRATGGCGT	480
CTGCAGTGT	TTTGTGATG	TTCTCCAGGC	ACAGGCTGGC	CAGCTGCGGT	TCATCGAAGA	540
GTCGCGCCTG	CGTGAGCAGC	ATGAAGGCCT	TGTCGGCTCG	CAGTTCTTCT	TCAGGAACTC	600
CACGCAAT						608

## (2) INFORMATION FOR SEQ ID NO:194:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

GAACGGCTGG	ACCTTGCCTC	GCATTGTGCT	TGCTGGCAGG	GAATACCTTG	GCAAGCAGYT	60
CCAGTCCGAG	CAGCCCCAGA	CCGCTGCCGC	CCGAAGCTAA	GCTGCCTCT	GGCCTTCCCC	120
TCCGCCTCAA	TGCAGAACCA	GTAGTGGGAG	CACTGTGTTT	AGAGTTAAGA	GTGAACACTG	180
TTTGATTTA	CTTGGGAATT	TCCTCTGTTA	TATAGCTTTT	CCCAATGCTA	ATTTCAAAC	240
AAACAACAACA	AAATAACATG	TTTGCCTGTT	AAGTTGTATA	AAAGTAGGTG	ATTCTGTATT	300
TAAGAAAAT	ATTACTGTTA	CATATACTGC	TTGCAATTTC	TGTATTTATT	GKTNCTSTGG	360
AAATAAAATAT	AGTTATTAAA	GGTTGTCANT	CC			392

## (2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

CCSTTKGAGG	GGTKAGGKYC	CAGTTYCCGA	GTGGAAGAAA	CAGGCCAGGA	GAAGTGC	GTG	60
CCGAGCTGAG	GCAGATGTT	CCACAGTGAC	CCCCAGAGCC	STGGG	STATA	GTYTCTGACC	120
CCTCNCAAGG	AAAGACCACS	TTCTGGGGAC	ATGGG	CTGGA	GGG	CAGGACC	180
AAGGGAAAGGC	CCCATTCCGG	GGSTGTTCCC	CGAGGAGGAA	GGGAAGGGC	TCTGTG	TGACC	240
CCCCASGAGG	AAGAGGCCCT	GAGTCCTGGG	ATCAGACACC	CCTTCACGTG	TAT	CCCCACA	300
CAAATGCAAG	CTCACCAAGG	TCCCCTCTCA	GTCCCCTTCC	STACACCCTG	AMCG	GGCCACT	360
GSCSCACACC	CACCCAGAGC	ACGCCACCCG	CCATGGGGAR	TGTGCTCAAG	GARTCG	CNGG	420
GCARCGTGGA	CATCTNGTCC	CAGAAGGGGG	CAGAATCTCC	AATAGANGGA	CTGARCM	STT	480
GCTNANAAAA	AAAAANAAAA	AA					502

## (2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 665 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

GGTTACTTGG	TTTCATTGCC	ACCACTTAGT	GGATGTCATT	TAGAACCATT	TTGTCTG	GTC	60	
CCTCTGGAAG	CCTTGC	GCAG	AGCGGACTTT	GTAATTGTTG	GAGAATAACT	GCTGA	120	
WAGCTGTTK	GAGTTGATT	GCACC	ACTGC	ACCCACA	ACT	TCAATATGAA	180	
ACTWATTTAT	TATCTTG	AAAGT	TATAAC	AATGAA	AA	AACYAWTTGA	240	
AAGTATGATG	AAAAGCAAWA	GATATAT	AT	CTTTTATT	AT	GTAAATTAT	300	
ATTAATCGGC	AAAATGTGG	GTG	TATGTT	TTTCACAGT	AAT	ATATATGCC	360	
TCAC	TTGGTT	ATTTTATTGT	AAATGARTTA	CAA	AAATTCTT	AATT	TAAGAR	420
WATATTTATT	TCATTA	ATTT	CTTCC	CTKGT	TTACG	TWAAT	TTGAAAAGA	480
TCTTGACAGA	AATCGAT	CTT	GATG	CTGTGG	AAGT	AGTTT	WTG	540
TTCTT	AGAAT	GTATAAAGGT	TCTAG	CCAT	CNA	ACTTC	CATG	600
TTT	GAATCA	GGCTGAAATG	TGG	CATG	CTAA	AGAAAAAAAT	GACCACATAC	660
AAGTG								665

## (2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

TTTTNTTTTT	TTTTTTTG	AGGAAGGATT	CCATTTATTG	TGGATGCATT	TTCACAATAT	60
ATGTTTATTG	GAGCGATCCA	TTATCACTGA	AAAGTATCAA	GTGTTTATAA	NATTTTCTAGG	120
AAGGCAGATT	CACAGAACAT	GCTNGTCNGC	TTGCAGTTTT	ACCTCGTANA	GATNACAGAG	180
AATTATAGTC	NAACCACTAA	ACNAGGAATT	TACTTTCAA	AAGATTAAAT	CCAAACTGAA	240
CAAAATTCTA	CCCTGAAACT	TACTCCATCC	AAATATTGGA	ATAANAGTC	GCAGTGATAC	300
ATTCTCTTCT	GAACTTAGA	TTTCTAGAA	AAATATGTAA	TAGTGATCAG	GAAGAGCTCT	360
TGTTCAAAAG	TACAACNAAG	CAATGTTCCC	TTACCATAGG	CCTTAATTCA	AACTTTGATC	420
CATTTCACTC	CCATCACGGG	AGTCAATGCT	ACCTGGGACA	CTTGTATTTT	GTTCATNCTG	480
ANCNTGGCTT	AA					492

## (2) INFORMATION FOR SEQ ID NO:198:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

TTTNTTTTGN	ATTCANTCT	GTANNAANTA	TTTCATTAT	GTATTATTANA	AAAATATNAA	60
TGNTCCACN	ACAAATCATN	TTACNTNAGT	AAGAGGCCAN	CTACATTGTA	CAACATACAC	120
TGAGTATATT	TTGAAAAGGA	CAAGTTAAA	GTANACNCAT	ATTGCCGANC	ATANCACATT	180
TATACATGGC	TTGATTGATA	TTTAGCACAG	CANAAACTGA	GTGAGTTACC	AGAAANAAAT	240
NATATATGTC	AATCNGATTT	AAGATACAAA	ACAGATCCTA	TGGTACATAN	CATCNTGTAG	300
GAGTTGTGGC	TTTATGTTA	CTGAAAGTCA	ATGCAGTTCC	TGTACAAAGA	GATGGCCGTA	360
AGCATTCTAG	TACCTCTACT	CCATGGTTAA	GAATCGTACA	CTTATGTTA	CATATGTNCA	420
GGGTAAGAAT	TGTGTTAAGT	NAANTTATGG	AGAGGTCCAN	GAGAAAATT	TGATNCAA	478

## (2) INFORMATION FOR SEQ ID NO:199:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

AGTGACTTGT	CCTCCAACAA	AACCCCTTGA	TCAAGTTGT	GGCACTGACA	ATCAGACCTA	60
TGCTAGTTCC	TGTCATCTAT	TCGCTACTAA	ATGCAGACTG	GAGGGGACCA	AAAAGGGCA	120
TCAACTCCAG	CTGGATTATT	TTGGAGCCTG	CAAATCTATT	CCTACTTGTA	CGGACTTTGA	180
AGTGATTCAG	TTTCCTCTAC	GGATGAGAGA	CTGGCTCAAG	AATATCCTCA	TGCAGCTTTA	240
TGAAGCCNAC	TCTGAACACG	CTGGTTATCT	NAGATGAGAA	NCAGAGAAAT	AAAGTCNAGA	300
AAATTTACCT	GGANGAAAAG	AGGCTTTNGG	CTGGGGACCA	TCCCATTGAA	CCTTCTCTTA	360
ANGGACTTTA	AGAANAAACT	ACCACATGTN	TGTNGTATCC	TGGTGCCNGG	CCGTTTANTG	420
AACNTNGACN	NCACCCTTNT	GGAAATANANT	CTTGACNGCN	TCCTGAACCTT	GCTCCTCTGC	480
GA						482

## (2) INFORMATION FOR SEQ ID NO:200:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

CGGCCGCAAG	TGCAACTCCA	GCTGGGGCCG	TGCGGACGAA	GATTCTGCCA	GCAGTTGGTC	60
CGACTCGGAC	GACGGCGGC	GCGACAGTCG	CAGGTGCAGC	GCGGGCGCCT	GGGGTCTTGC	120
AAGGCTGAGC	TGACGCCGCA	GAGGTCTGTG	CACGTCCCAC	GACCTTGACG	CCGTGGGGAA	180
CAGCCGGAAC	AGAGCCCCGGT	GAANGCGGG	GGCCTCGGGG	AGCCCCTCGG	GAAGGGCGGC	240
CCGAGAGATA	CGCAGGTGCA	GGTGGCCG				270

## (2) INFORMATION FOR SEQ ID NO:201:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

TTTTTTTTTT	TTTTGGAATC	TACTGCGAGC	ACAGCAGGTC	AGCAACAAGT	TTATTTGCA	60
GCTAGCAAGG	TAACAGGGTA	GGGCATGGTT	ACATGTTAG	GTCAACTTC	TTTGTCTGG	120
TTGATTGGTT	TGTCTTATG	GGGGCGGGGT	GGGGTAGGGG	AAANCGAAGC	ANAAANTAAACA	180
TGGAGTGGGT	GCACCCCTCCC	TGTAGAACCT	GGTTACNAAA	GCTTGGGGCA	GTTCACCTGG	240
TCTGTGACCG	TCATTTCTT	GACATCAATG	TTATTAGAAG	TCAGGATATC	TTTTAGAGAG	300
TCCACTGTNT	CTGGAGGGAG	ATTAGGGTTT	CTTGCCAANA	TCCAANCAA	ATCCACNTGA	360
AAAAGTTGGA	TGATNCANGT	ACNGAATACC	GANGGCATAN	TTCTCATANT	CGGTGGCCA	419

## (2) INFORMATION FOR SEQ ID NO:202:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

TTTNTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	60
TGGCACTTAA	TCCATTTTA	TTTCAAATG	TCTACAAANT	TTNAATNCNC	CATTATACNG	120
GTNAITTTNC	AAAATCTAAA	NNTTATTCAA	ATNTNAGCCA	AANTCCTTAC	NCAAATNAA	180
TACNCNAAA	AATCAAAAAT	ATACNTNTCT	TTCAGCAAAC	TNGTTACAT	AAATTAAAAAA	240
AATATATACG	GCTGGTGT	TCAAAGTACA	ATTATCTTAA	CACTGCAAAC	ATNTTNNAA	300
GGAACTAAAA	TAAAAAAA	CACTNCCGCA	AAGGTAAAG	GGAACAACAA	ATTCTNTTAA	360
CAACACNCNC	NATTAAAAA	ATCATATCTC	AAATCTTAGG	GGAATATATA	CTTCACACNG	420
GGATCTTAAC	TTTTACTNCA	CTTGTGTTAT	TTTTTANAA	CCATTGTNTT	GGGCCAAACA	480
CAATGGNAAT	NCCNCNCNC	TGGACTAGT				509

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

TTTTNTTTT	TTTTTTTGC	AGGAAGGATT	CCATTTATTG	TGGATGCATT	TTCACAATAT	60
ATGTTTATTG	GAGCGATCCA	TTATCAGTGA	AAAGTATCAA	GTGTTTATAA	NATTTTAGG	120
AAGGCAGATT	CACAGAACAT	GCTNGTCNGC	TTGCAGTTT	ACCTCGTANA	GATNACAGAG	180
AATTATAGTC	NAACCAGTAA	ACNAGGAATT	TACTTTCAA	AAGATTAAT	CCAAACTGAA	240
CAAAATTCTA	CCCTGAAACT	TACTCCATCC	AAATATTGGA	ATAANAGTCA	GCAGTGATAC	300
ATTCTCTTCT	GAACTTAGA	TTTCTAGAA	AAATATGTAA	TAGTGATCAG	GAAGAGCTCT	360
TGTTCAAAAG	TACAACNAAG	CAATGTTCCC	TTACCATAGG	CCTTAATTCA	AACTTTGATC	420
CAITTCACTC	CCATCACGGG	AGTCAATGCT	ACCTGGGACA	CTTGTATTTC	GTTCATNCTG	480
ANCNTGGCTT	AA					492

## (2) INFORMATION FOR SEQ ID NO:198:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

TTTNTTTTGN	ATTCANTCT	GTANNAANTA	TTTCATTAT	GTATTATTANA	AAAATATNAA	60
TGTNTCCACN	ACAAATCATN	TTACNTNAGT	AAGAGGCCAN	CTACATTGTA	CAACATACAC	120
TGAGTATATT	TTGAAAAGGA	CAAGTTAAA	GTANACNCAT	ATTGCCGANC	ATANCACATT	180
TATACATGGC	TTGATTGATA	TTTAGCACAG	CANAAACTGA	GTGAGTTACC	AGAAANAAAT	240
NATATATGTC	AATCNGATT	AAGATACAAA	ACAGATCCTA	TGGTACATAN	CATCNTGTAG	300
GAGTTGTGGC	TTTATGTTA	CTGAAAGTCA	ATGCAGTTCC	TGACAAAGA	GATGGCCGTA	360
AGCATTCTAG	TACCTCTACT	CCATGGTTAA	GAATCGTACA	CTTATGTTA	CATATGTNCA	420
GGGTAAAGAAT	TGTGTTAAGT	NAANTTATGG	AGAGGTCCAN	GAGAAAATT	TGATNCAA	478

## (2) INFORMATION FOR SEQ ID NO:199:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

AGTGACTTGT	CCTCCAACAA	AACCCCTTGA	TCAAGTTTGT	GGCACTGACA	ATCAGACCTA	60
TGCTAGTTCC	TGTCATCTAT	TCGCTACTAA	ATGCAGACTG	GAGGGGACCA	AAAAGGGCA	120
TCAACTCCAG	CTGGATTATT	TTGGAGCTG	CAAATCTATT	CCTACTTGT	CGGACTTTGA	180
AGTGATTCAG	TTTCCTCTAC	GGATGAGAGA	CTGGCTCAAG	AATATCCTCA	TGCAGCTTTA	240
TGAAGCCNAC	TCTGAACACG	CTGGTTATCT	NAGATGAGAA	NCAGAGAAAT	AAAGTCNAGA	300
AAATTTACCT	GGANGAAAAG	AGGCTTNGG	CTGGGGACCA	TCCCATTGAA	CCTTCTCTTA	360
ANGGACTTTA	AGAANAAACT	ACCACATGTN	TGTNGTATCC	TGGTGCCNGG	CCGTTTANTG	420
AACNTNGACN	NCACCCTNT	GGAATANANT	CTTGACNGCN	TCCTGAACCTT	GCTCCTCTGC	480
GA						482

## (2) INFORMATION FOR SEQ ID NO:200:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

CGGCGCGAAG	TGCAACTCCA	GCTGGGGCCG	TGCGGACGAA	GATTCTGCCA	GCAGTTGGTC	60
CGACTGCGAC	GACGGCGCG	GCGACAGTCG	CAGGTGCAGC	GCGGGCGCCT	GGGGTCTTGC	120
AAGGCTGAGC	TGACGCCGCA	GAGGTCGTGT	CACGTCCCAC	GACCTTGACG	CCGTCGGGGA	180
CAGCCGGAAC	AGACCCCCGT	GAANGCGGA	GGCCTCGGG	AGCCCCTCGG	GAAGGGCGGC	240
CCGAGAGATA	CGCAGGTGCA	GGTGGCCGCG				270

## (2) INFORMATION FOR SEQ ID NO:201:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

TTTTTTTTTT	TTTTGGAATC	TACTGCGAGC	ACAGCAGGTC	AGCAACAAGT	TTATTTGCA	60
GCTAGCAAGG	TAACAGGGTA	GGGCATGGTT	ACATGTTCA	GTCAACTTCC	TTTGTCTG	120
TTGATTGGTT	TGTCTTATG	GGGGCGGGGT	GGGGTAGGGG	AAANCGAAGC	ANAANTAA	180
TGGAGTGGGT	GCACCCCTCCC	TGTAGAACCT	GGTTACNAAA	GCTTGGGGCA	GTTCACCTGG	240
TCTGTGACCG	TCATTTCTT	GACATCAATG	TTATTAGAAC	TCAGGATATC	TTTTAGAGAG	300
TCCACTGTNT	CTGGAGGGAG	ATTAGGGTTT	CTTGCCAANA	TCCAANAAA	ATCCACNTGA	360
AAAAGTTGGA	TGATNCANGT	ACNGAATACC	GANGGCATAN	TTCTCATANT	CGGTGGCCA	419

## (2) INFORMATION FOR SEQ ID NO:202:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

TTTNTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	60
TGGCACTTAA	TCCATTNTTA	TTCAAAATG	TCTACAAANT	TTNAATNCNC	CATTATAACNG	120
GTNATTNTNC	AAAATCTAA	NNTTATTCAA	ATNTNAGCCA	AANTCCTTAC	NCAAATNNA	180
TACNCNCAA	AATCAAAAT	ATACNTNTCT	TTCAGCAAAC	TTNGTTACAT	AAATTAAAAA	240
AATATATACG	GCTGGTGT	TCAAAGTACA	ATTATCTTAA	CACTGCAAAC	ATNTTTNNA	300
GGAACTAAA	AAAAAA	CACTNCCGCA	AAGGTTAAAG	GGAAACAACAA	ATTCNTTTA	360
CAACANCNC	NATTATAAA	ATCATATCTC	AAATCTTAGG	GGAAATATATA	CTTCACACNG	420
GGATCTTAAC	TTTACTNCA	CTTTGTTTAT	TTTTTANAA	CCATTGTNTT	GGGCCAAACA	480
CAATGGNAAT	NCCNCCNCC	TGGACTAGT				509

## (2) INFORMATION FOR SEQ ID NO:203:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 583 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

TTTTTTTTTT	TTTTTTTG	CCCCCTCTT	ATAAAAAACA	AGTTACCATT	TTATTTTACT	60
TACACATATT	TATTTTATAA	TTGGTATTAG	ATATTCAAAA	GGCAGCTTT	AAAATCAAAC	120
TAAATGGAAA	CTGCCTTAGA	TACATAATT	TTAGGAATT	GCTTAAAATC	TGCCTAAAGT	180
AAAAATCTTC	TCTAGCTCTT	TTGACTGTAA	ATTTTGACT	CTTGTAAAAC	ATCCAAATTC	240
ATTTTCTTG	TCTTTAAAT	TATCTAATCT	TTCCATT	TCCCTATTCC	AAGTCAATT	300
GCTTCTCTAG	CCTCATTCC	TAGCTTTAT	CTACTATTAG	TAAGTGGCTT	TTTTCTAAA	360
AGGGAAAACA	GGAAGAGANA	ATGGCACACA	AAACAAACAT	TTTATATTCA	TATTTCTACC	420
TACGTTAATA	AAATAGCATT	TTGTGAAGCC	AGCTAAAAG	AAGGCTTAGA	TCCTTTATG	480
TCCATT	TCACTAAACG	ATATCNAAG	TGCCAGAATG	CAAAGGTTT	GTGAACATT	540
ATTCAAAAGC	TAATATAAGA	TATTCACAT	ACTCATCTT	CTG		583

## (2) INFORMATION FOR SEQ ID NO:204:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 589 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

TTTTTTTTNT	TTTTTTTTTT	TTTTTNCTC	TTCTTTTTTT	TTGANAATGA	GGATCGAGTT	60
TTTCACTCTC	TAGATAGGGC	ATGAAGAAA	CTCATCTTC	CAGCTTTAAA	ATAACAATCA	120
AATCTCTTAT	GCTATATCAT	ATTTAAGTT	AAACTAATGA	GTCACTGGCT	TATCTTCTCC	180
TGAAGGAAAT	CTGTTCATTC	TTCTCATTCA	TATAGTTATA	TCAAGTACTA	CCTTGCATAT	240
TGAGAGGTTT	TTCTTCTCTA	TTTACACATA	TATTTCCATG	TGAATTGTA	TCAAACCTT	300
ATTTTCATGC	AAACTAGAAA	ATAATGTNTT	CTTTGCATA	AGAGAAGAGA	ACAATATNAG	360
CATTACAAAA	CTGCTAAAT	TGTTGTTAA	GNTTATCCAT	TATAATTAGT	TNGGCAGGAG	420
CTAATACAAA	TCACATTTAC	NGACNAGCAA	TAATAAAACT	GAAGTACCAAG	TTAAATATCC	480
AAAATAATTA	AAGGAACATT	TTAGCCTGG	GTATAATTAG	CTAATTCACT	TTACAAGCAT	540
TTATTNAGAA	TGAATTCA	TGTTATTATT	CCNTAGCCC	ACACAATGG		589

## (2) INFORMATION FOR SEQ ID NO:205:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

TTTTTNTTTT TTTTTTCAGT AATAATCAGA ACAATATTAA TTTTTATATT TAAAATTCA	60
AGAAAAGTGC CTTACATTAA ATAAAAGTTT GTTCTCAAA GTGATCAGAG GAATTAGATA	120
TNGTCTTGAA CACCAATATT AATTTGAGGA AAATACACCA AAATACATTA AGTAAATTAT	180
TTAAGATCAT AGAGCTTGTA AGTAAAAGA TAAAATTGA CCTCAGAAC TCTGAGCATT	240
AAAAATCCAC TATTAGCAAA TAAATTACTA TGGACTTCTT GCTTTAATTG TGTGATGAAT	300
ATGGGGTGTGTC ACTGGTAAAC CAACACATTC TGAAGGATAC ATTACTTAGT GATAGATTCT	360
TATGTACTTT GCTANATNAC GTGGATATGA GTTGACAAGT TTCTCTTCT TCAATCTTT	420
AAGGGCNGA NGAAATGAGG AAGAAAAGA AAGGATTACG CATACTGTTC TTTCTATNGG	480
AAGGATTAGA TATGTTTCCT TTGCCAATAT TAAAAAAATA ATAATGTTA CTACTAGTGA	540
AACCC	545

## (2) INFORMATION FOR SEQ ID NO:206:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

TTTTTTTTTTT TTTTTTAGTC AAGTTCTNA TTTTTATTAT AATTAAAGTC TTGGTCATTT	60
CATTTATTAG CTCTGCAACT TACATATTAA AATTAAAGAA ACGTTNTTAG ACAACTGTNA	120
CAATTATAA ATGTAAGGTG CCATTATTGA GTANATATAT TCCTCCAAGA GTGGATGTGT	180
CCCTTCTCCC ACCAACTAAT GAANCAGCAA CATTAGTTA ATTTTATTAG TAGATNATAC	240
ACTGCTGCAA ACGCTAATTTC TCTTCTCCAT CCCCAGTNG ATATTGTGTA TATGTGTGAG	300
TTGGTNAGAA TGCATCANCA ATCTNACAAT CAACAGCAAG ATGAAGCTAG GCNTGGGCTT	360
TCGGTAAAAA TAGACTGTGT CTGTCTGAAT CAAATGATCT GACCTATCCT CGGTGGCAAG	420
AACTCTTCGA ACCGCTTCCT CAAAGGCNGC TGCCACATTT GTGGCNTCTN TTGCACTTGT	480
TTCAAAA	487

## (2) INFORMATION FOR SEQ ID NO:207:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

TGAATTGGCT AAAAGACTGC ATTTTTANAA CTAGCAACTC TTATTTCTTT CCTTTAAAAAA	60
TACATAGCAT TAAATCCCAA ATCCTATTAA AAGACCTGAC AGCTTGAGAA GGTCACTACT	120
GCATTTATAG GACCTTCTGG TGGTTCTGCT GTTACNTTTG AANTCTGACA ATCCTTGANA	180
ATCTTTGCAT GCAGAGGAGG TAAAAGGTAT TGGATTITCA CAGAGGAANA ACACAGCGCA	240
GAAATGAAGG GGCCAGGCTT ACTGAGCTG TCCACTGGAG GGCTCATGGG TGGGACATGG	300
AAAAGAAGGC AGCCTAGGCC CTGGGGAGCC CA	332

## (2) INFORMATION FOR SEQ ID NO:208:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 524 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

AGGGCGTGGT GCGGAGGGCG TTACTGTTT GTCTCAGTAA CAATAAATAC AAAAAGACTG	60
GTTGTGTTCC GGCCCCATCC AACACAGAAG TTGATTTCTC TTGTGTGCAG AGTGACTGAT	120
TTTAAAGGAC ATGGAGCTTG TCACAAATGTC ACAATGTCAC AGTGTGAAGG GCACACTCAC	180
TCCCGCGTGA TTCACATTAA GCAACCAACA ATAGCTCATG AGTCCATACT TGAAATACT	240
TTTGGCAGAA TACTTNTTGA AACCTTGAGA TGATAACTAA GATCCAAGAT ATTTCCCAA	300
GTAAATAGAA GTGGGTCATA ATATTAATTAA CCTGTTACAA TCAGCTTCCA TTTACAAGTC	360
ATGAGCCCAG ACACTGACAT CAAACTAAGC CCACTTAGAC TCCTCACCAC CAGTCTGTCC	420
TGTACATCAGA CAGGAGGCTG TCACCTTGAC CAAATTCTCA CCAGTCAAATC ATCTATCAA	480
AAACCATTAC CTGATCCACT TCCGGAATG CACCACCTTG GTGA	524

(2) INFORMATION FOR SEQ ID NO:209:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 159 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

GGGTGAGGAA ATCCAGAGTT GCCATGGAGA AAATTCCAGT GTCAGCATTG TTGCTCCTTG	60
TGGCCCTCTC CTACACTCTG GCCAGAGATA CCACAGTCAA ACCTGGAGCC AAAAAGGACA	120
CAAAGGACTC TCGACCCAAA CTGCCCCAGA CCCTCTCCA	159

(2) INFORMATION FOR SEQ ID NO:210:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

ACTCCCTGGC AGACAAAGGC AGAGGGAGAGA GCTCTGTTAG TTCTGTGTTG TTGAACTGCC	60
ACTGAATTTC TTTCCACTTG GACTATTACA TGCCANTGAA GGGACTAATG GAAAAACGTA	120
TGGGGAGATT TTANCCAATT TANGNTGTA AATGGGGAGA CTGGGGCAGG CGGGAGAGAT	180
TTGCAGGGTG NAAATGGGAN GGCTGGTTTG TTANATGAAC AGGGACATAG GAGGTAGGCA	240
CCAGGATGCT AAATCA	256

(2) INFORMATION FOR SEQ ID NO:211:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

ACATTGTTTT TTTGAGATAA AGCATTGAGA GAGCTCTCCT TAACGTGACA CAATGGAAGG	60
ACTGGAACAC ATACCCACAT CTTTGTCTG AGGGATAATT TTCTGATAAA GTCTTGCTGT	120
ATATTCAAGC ACATATGTTA TATATTATTC AGTTCATGT TTATAGCCTA GTTAAGGAGA	180
GGGGAGATAAC ATTNCNGAAAG AGGACTGAAA GAAATACTCA AGTNGGAAAA CAGAAAAAGA	240
AAAAAAGGAG CAAATGAGAA GCCT	264

## (2) INFORMATION FOR SEQ ID NO:212:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

ACCCAAAAAT CCAATGCTGA ATATTTGGCT TCATTATTCC CANATTCTTT GATTGTCAAA	60
GGATTTAACG TTGTCAGC TTGGGCACCT CAGTTAGGAC CTAAGGATGC CAGCCGGCAG	120
GTTTATATAT GCAGCAACAA TATTCAAGCG CGACAAACAGG TTATTGAAC TGCCCGCCAG	180
TTAAATTTCAT TTCCCATTGA CTTGGGATCC TTATCATCG CCAGAGAGAT TGAAAATTAA	240
CCCTTACNAC TCTTTACTCT CTGGANAGGG CCAGTGGTGG TAGCTATAAG CTTGGCCACAA	300
TTTTTTTTTC CTTTATTCCCT TTGTCAGA	328

## (2) INFORMATION FOR SEQ ID NO:213:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

ACTTATGAGC AGAGCGACAT ATCCNAGTGT AGACTGAATA AACTGAATT CTCTCCAGTT	60
TAAAGCATTG CTCACTGAAG GGATAGAAGT GACTGCCAGG AGGGAAAGTA AGCCAAGGCT	120
CATTATGCCA AAGGANATAT ACATTTCAAT TCTCCAAACT TCTTCCTCAT TCCAAGAGTT	180
TTCAATATTT GCATGAACCT GCTGATAANC CATGTTAANA AACAAATATC TCTCTNACCT	240
TCTCATCGGT	250

## (2) INFORMATION FOR SEQ ID NO:214:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

ACCCAGAACAT	CAATGCTGAA	TATTTGGCTT	CATTATTCCC	AGATTCTTG	ATTGTCAAAG	60
GATTTAATGT	TGTCTCAGCT	TGGGCACCTC	AGTTAGGACC	TAAGGATGCC	AGCCGGCAGG	120
TTTATATATG	CAGCAACAAT	ATTCAAGCGC	GACAACAGGT	TATTGAACCT	GCCCCGCCAGT	180
TGAATTTCAT	TCCCATTGAC	TTGGGATCCT	TATCATCAGC	CANAGAGATT	GAAAATTAC	240
CCCTACGACT	CTTTACTCTC	TGGAGAGGGC	CAGTGGTGGT	AGCTATAAGC	TTGGCCACAT	300
TTTTTTTCTC	TTTATTCCCT	TGTCAGAGAT	GCGATTCAATC	CATATGCTAN	AAACCAACAG	360
AGTACTTTT	ACAAAATTCC	TATAGANATT	GTGAATAAAA	CCTTACCTAT	AGTTGCCATT	420
ACTTTGCTCT	CCCTAACATA	CCTC				444

## (2) INFORMATION FOR SEQ ID NO:215:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

ACTTATGAGC	AGAGCGACAT	ATCCAAGTGT	ANACTGAATA	AAACTGAATT	CTCTCCAGTT	60
TAAAGCATTG	CTCACTGAAG	GGATAGAACT	GACTGCCAGG	AGGGAAAGTA	AGCCAAGGCT	120
CATTATGCCA	AAGGANATAT	ACATTCAAT	TCTCCAAACT	TCTTCCTCAT	TCCAAGAGTT	180
TTCAATATTT	GCATGAACCT	GCTGATAAGC	CATGTTGAGA	AACAAATATC	TCTCTGACCT	240
TCTCATCGGT	AAGCAGAGGC	TGTAGGCAAC	ATGGACCATA	GCGAANAAAA	AACTTAGTAA	300
TCCAAGCTGT	TTTCTACACT	GTAACCAGGT	TTCCAACCAA	GGTGGAAATC	TCCTATACTT	360
GGTGCC						366

## (2) INFORMATION FOR SEQ ID NO:216:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

CTGTATAAAC	AGAACTCCAC	TGCANGAGGG	AGGGCCGGGC	CAGGAGAACAT	TCCGCTTGTC	60
CAAGACAGGG	GCCTAAAGGAG	GGTCTCCACA	CTGCTNNNTAA	GGGCTNTTNC	ATTTTTTTAT	120
TAATAAAAAG	TNNAAAAGGC	CTCTTCTCAA	CTTTTTCCC	TTNGGCTGGA	AAATTTAAAAA	180
ATCAAAATT	TCCTNAAGTT	NTCAAGCTAT	CATATATACT	NTATCCTGAA	AAAGCAACAT	240

AATTCTTCCT TCCCTCCTTT

260

## (2) INFORMATION FOR SEQ ID NO:217:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

ACCTACGTGG GTAAGTTTAN AAATGTTATA ATTCAGGAA NAGGAACGCA TATAATTGTA	60
TCTTGCTAT AATTTCTAT TTTAATAAGG AAATAGCAAA TTGGGGTGGG GGGATGTAG	120
GGCATTCTAC AGTTTGAGCA AAATGCAATT AAATGTGGAA GGACAGCACT GAAAAATTAA	180
ATGAATAATC TGTATGATTA TATGTCTCTA GAGTAGATT ATAATTAGCC ACTTACCCCTA	240
ATATCCTTCA TGCTTGTAAA GT	262

## (2) INFORMATION FOR SEQ ID NO:218:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

ACCAAGGTGG TGCATTACCG GAANTGGATC AANGACACCA TCGTGGCCAA CCCCTGAGCA	60
CCCCTATCAA CTCCCTTTTG TAGTAAACCTT GGAACCTTGG AAATGACCAAG GCCAAGACTC	120
AGGCCTCCCC AGTTCTACTG ACCTTTGTCC TTANGTNTNA NGTCCAGGGT TGCTAGGAAA	180
ANAAAATCAGC AGACACAGGT GTAAA	205

## (2) INFORMATION FOR SEQ ID NO:219:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

TACTGTTTTG TCTCAGTAAC AATAAAATACA AAAAGACTGG TTGTGTTCCG GCCCCATCCA	60
ACCACGAAGT TGATTTCTCT TGTGTGCAGA GTGACTGATT TTAAAGGACA TGGA	114

## (2) INFORMATION FOR SEQ ID NO:220:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

ACTAGCCAGC ACAAAAGGCA GGGTAGCCTG AATTGCTTTC TGCTCTTAC ATTTCTTTA 60  
AAATAAGCAT TTAGTGTCA GTCCCTACTG AGT 93

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

ACTANGTGCA GGTGGCACA AATATTTGTC GATATTCCCT TCATCTTGGA TTCCATGAGG 60  
TCTTTGCCA AGCCTGTGGC TCTACTGTAG TAAGTTCTG CTGATGAGGA GCCAGNATGC 120  
CCCCCACTAC CTTCCCTGAC GCTCCCCANA AATCACCCAA CCTCTGT 167

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

AGGGCGTGGT GCGGAGGGCG GTACTGACCT CATTAGTAGG AGGATGCATT CTGGCACCC 60  
GTTCTTCACC TGTCCCCAA TCCTTAAAG GCCATACTGC ATAAAGTCAA CAACAGATAA 120  
ATGTTTGCTG AATTAAAGGA TGGATGAAAA AAATTAATAA TGAATTTTG CATAATCCAA 180  
TTTTCTCTTT TATATTCTA GAAGAAGTTT CTTTGAGCCT ATTAGATCCC GGGAAATCTTT 240  
TAGGTGAGCA TGATTAGAGA GCTTGTAGGT TGCTTTACA TATATCTGGC ATATTGAGT 300  
CTCGTATCAA AACAAATAGAT TGGTAAAGGT GGTATTATTG TATTGATAAG T 351

(2) INFORMATION FOR SEQ ID NO:223

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

AAAACAAACA AACAAAAAAA ACAATTCTTC ATTCAAGAAAA ATTATCTTAG GGACTGATAT	60
TGGTAATTAT GGTCAATTAA ATWRTRTTKT GGGGCATTTC CTTACATTGT CTTGACAAGA	120
TTAAAATGTC TGTGCCAAAA TTTTGTATT TATTTGGAGA CTTCTTATCA AAAGTAATGC	180
TGCCAAAGGA AGTCTAAGGA ATTAGTAGTG TTCCCMTCAC TTGTTGGAG TGTGCTATT	240
TAAAAGATT TGATITCCTG GAATGACAAT TATATTTAA CTTTGGTGGG GGAAANAGTT	300
ATAGGACCAAC AGTCTCACT TCTGATACTT GTAAATTAAT CTTTATTGC ACTTGTGTTG	360
ACCATTAAGC TATATGTTA AAA	383

## (2) INFORMATION FOR SEQ ID NO:224

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:224

CCCCCTGAAGG CTTCTTGTAA GAAAATAGTA CAGTTACAAC CAATAGGAAC AACAAAAAGA	60
AAAAGTTTGT GACATTGTAG TAGGGAGTGT GTACCCCTTA CTCCCCATCA AAAAAAAAAT	120
GGATACATGG TTAAAGGATA RAAGGGCAAT ATTTTATCAT ATGTTCTAAA AGAGAAGGAA	180
GAGAAAATAC TACTTCTCR AAATGGAAGC CCTTAAAGGT GCTTGATAC TGAAGGACAC	240
AAATGTGGCC GTCCATCCTC CTTTARAGTT GCATGACTTG GACACGGTAA CTGTTGCAGT	300
TTTARACTCM GCATTGTGAC	320

## CLAIMS

1. A method for detecting prostate cancer in a patient, comprising:
  - (a) contacting a biological sample obtained from the patient with a binding agent which is capable of binding to a polypeptide, the polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences and variants of said nucleotide sequences; and
  - (b) detecting in the sample a protein or polypeptide that binds to the binding agent, thereby detecting prostate cancer in the patient.
2. The method of claim 1 wherein the binding agent is a monoclonal antibody.
3. The method of claim 2 wherein the binding agent is a polyclonal antibody.
4. A method for monitoring the progression of prostate cancer in a patient, comprising:
  - (a) contacting a biological sample obtained from the patient with a binding agent that is capable of binding to a polypeptide, said polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences and variants of said nucleotide sequences;
  - (b) determining in the sample an amount of a protein or polypeptide that binds to the binding agent;
  - (c) repeating steps (a) and (b); and

(d) comparing the amount of polypeptide detected in steps (b) and (c) to monitor the progression of prostate cancer in the patient.

5. A monoclonal antibody that binds to a polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 8-29, 41-45, 47-52, 54-65, 70, 73, 74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209-211, 220, 222-224, the complements of said nucleotide sequences variants of said nucleotide sequences.

6. A method for inhibiting the development of prostate cancer in a patient, comprising administering to the patient a therapeutically effective amount of a monoclonal antibody according to claim 5.

7. The method of claim 6 wherein the monoclonal antibody is conjugated to a therapeutic agent.

8. A method for detecting prostate cancer in a patient comprising:

- (a) obtaining a biological sample from the patient;
- (b) contacting the sample with at least two oligonucleotide primers in a polymerase chain reaction, wherein at least one of the oligonucleotides is specific for a DNA molecule encoding a polypeptide comprising an immunogenic portion of a prostate protein or of a variant thereof, said protein comprising an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences variants of said nucleotide sequences; and
- (c) detecting in the sample a DNA sequence that amplifies in the presence of the oligonucleotide primers, thereby detecting prostate cancer.

9. The method of claim 8, wherein at least one of the oligonucleotide primers comprises at least about 10 contiguous nucleotides of a DNA molecule having a sequence selected from SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224.

10. A diagnostic kit comprising:

- (a) one or more monoclonal antibodies of claim 5; and
- (b) a detection reagent.

11. A diagnostic kit comprising:

- (a) one or more monoclonal antibodies that bind to a polypeptide encoded by a DNA molecule having a nucleotide sequence selected from the group consisting of SEQ ID Nos: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106, 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219, 221, the complements of said sequences and variants of said nucleotide sequences; and
- (b) a detection reagent.

12. The kit of claims 10 or 11 wherein the monoclonal antibodies are immobilized on a solid support.

13. The kit of claim 12 wherein the solid support comprises nitrocellulose, latex or a plastic material.

14. The kit of claims 10 or 11 wherein the detection reagent comprises a reporter group conjugated to a binding agent.

15. The kit of claim 14 wherein the binding agent is selected from the group consisting of anti-immunoglobulins, Protein G, Protein A and lectins.

16. The kit of claim 14 wherein the reporter group is selected from the group consisting of radioisotopes, fluorescent groups, luminescent groups, enzymes, biotin and dye particles.

17. A diagnostic kit comprising at least two oligonucleotide primers, at least one of the oligonucleotide primers being specific for a DNA molecule encoding a polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, said protein comprising an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences and variants of said nucleotide sequences.

18. A diagnostic kit of claim 17 wherein at least one of the oligonucleotide primers comprises at least about 10 contiguous nucleotides of a DNA molecule having a sequence selected from SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224.

19. A method for detecting prostate cancer in a patient, comprising:

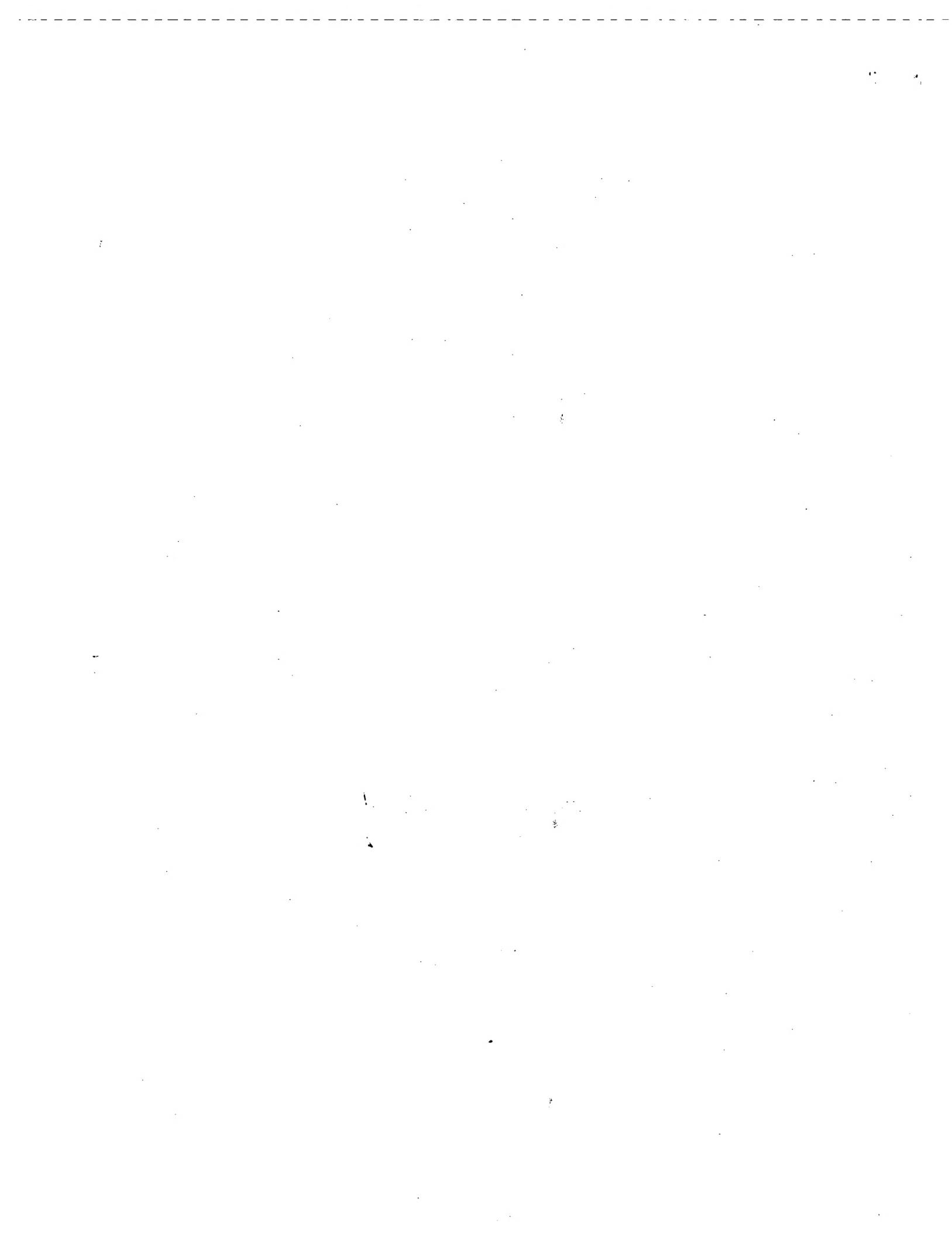
- (a) obtaining a biological sample from the patient;
- (b) contacting the biological sample with an oligonucleotide probe specific for a DNA molecule encoding a polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, said protein comprising an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences and variants of said nucleotide sequences; and
- (c) detecting in the sample a DNA sequence that hybridizes to the oligonucleotide probe, thereby detecting prostate cancer in the patient.

20. The method of claim 19 wherein the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA molecule having a sequence selected from the group consisting of SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224.

21. A diagnostic kit comprising an oligonucleotide probe specific for a DNA molecule encoding a polypeptide comprising an immunogenic portion of a prostate

protein or a variant thereof, said protein comprising an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences variants of said nucleotide sequences.

22. The diagnostic kit of claim 21, wherein the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA molecule having a sequence selected from the group consisting of SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224.





## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification <sup>6</sup> : <b>G01N 33/574, 33/577, C07K 16/30, A61K 39/395, 47/48, C12Q 1/68, G01N 33/543</b>		A2	(11) International Publication Number: <b>WO 98/37418</b>
			(43) International Publication Date: <b>27 August 1998 (27.08.98)</b>
(21) International Application Number: <b>PCT/US98/03690</b>			(81) Designated States: AL, AM, AT, AU, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).
(22) International Filing Date: <b>25 February 1998 (25.02.98)</b>			
(30) Priority Data:			
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08/904,809	1 August 1997 (01.08.97)	US	
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(71) Applicant: CORIXA CORPORATION [US/US]; Suite 200, 1124 Columbia Street, Seattle, WA 98104 (US).			<b>Published</b> <i>Without international search report and to be republished upon receipt of that report.</i>
(72) Inventors: XU, Jiangchun; 15805 Southeast 43rd Place, Bellevue, WA 98006 (US). DILLON, Davin, C.; 21607 N.E. 24th Street, Redmond, WA 98053 (US).			
(74) Agents: MAKI, David, J. et al.; Seed and Berry LLP, 6300 Columbia Center, 701 Fifth Avenue, Seattle, WA 98104-7092 (US).			

(54) Title: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS FOR THEIR USE

## (57) Abstract

Compounds and methods for diagnosing prostate cancer are provided. The inventive compounds include polypeptides containing at least a portion of a prostate tumor protein. The inventive polypeptides may be used to generate antibodies useful for the diagnosis and monitoring of prostate cancer. Nucleic acid sequences for preparing probes, primers, and polypeptides are also provided.

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(51) International Patent Classification <sup>6</sup> : <b>G01N 33/574, 33/577, C07K 16/30, A61K 39/395, 47/48, C12Q 1/68, G01N 33/543</b>		A3	(11) International Publication Number: <b>WO 98/37418</b> (43) International Publication Date: <b>27 August 1998 (27.08.98)</b>
(21) International Application Number: <b>PCT/US98/03690</b>		(81) Designated States: AL, AM, AT, AU, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).	
(22) International Filing Date: <b>25 February 1998 (25.02.98)</b>			
(30) Priority Data: 08/806,596 25 February 1997 (25.02.97) US 08/904,809 1 August 1997 (01.08.97) US 09/020,747 9 February 1998 (09.02.98) US			
(71) Applicant: CORIXA CORPORATION [US/US]; Suite 200, 1124 Columbia Street, Seattle, WA 98104 (US).		Published <i>With international search report. Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i>	
(72) Inventors: XU, Jiangchun; 15805 Southeast 43rd Place, Bellevue, WA 98006 (US). DILLON, Davin, C.; 21607 N.E. 24th Street, Redmond, WA 98053 (US).		(88) Date of publication of the international search report: <b>25 February 1999 (25.02.99)</b>	
(74) Agents: MAKI, David, J. et al.; Seed and Berry LLP, 6300 Columbia Center, 701 Fifth Avenue, Seattle, WA 98104-7092 (US).			

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## (57) Abstract

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## INTERNATIONAL SEARCH REPORT

International Application No

PC., US 98/03690

## A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 G01N33/574 G01N33/577 G01N33/543 C07K16/30 C12Q1/68  
A61K39/395 A61K47/48

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12Q C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WO 96 21671 A (UNIV COLUMBIA ;FISHER PAUL B (US); SHEN RUOQUIAN (US)) 18 July 1996 see the whole document ---	1-10, 12-22
A	EL-SHIRBINY A M: "PROSTATIC SPECIFIC ANTIGEN" ADVANCES IN CLINICAL CHEMISTRY, vol. 31, 1994, pages 99-133, XP000617158 see the whole document ---	1-10, 12-22
A	WO 93 14775 A (WRIGHT GEORGE L JR) 5 August 1993 see the whole document ---	1-10, 12-22

 Further documents are listed in the continuation of box C. Patent family members are listed in annex.

## \* Special categories of cited documents :

- \*A\* document defining the general state of the art which is not considered to be of particular relevance
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Date of the actual completion of the international search

31 August 1998

Date of mailing of the international search report

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## INTERNATIONAL SEARCH REPORT

International Application No

PCT/JS 98/03690

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WO 94 09820 A (SLOAN KETTERING INST CANCER ; ISRAELI RON S (US); HESTON WARREN D W) 11 May 1994 see the whole document ---	1-10, 12-22
A	WO 95 04548 A (JENNER TECHNOLOGIES) 16 February 1995 see the whole document ---	1-10, 12-22
A	ROBSON C N ET AL: "IDENTIFICATION OF PROSTATIC ANDROGEN REGULATED GENES USING THE DIFFERENTIAL DISPLAY TECHNIQUE" PROCEEDINGS OF THE ANNUAL MEETING OF THE AMERICAN ASSOCIATION FOR CANCER RESEARCH, TORONTO, MAR. 18 - 22, 1995, no. MEETING 86, 18 March 1995, AMERICAN ASSOCIATION FOR CANCER RESEARCH, page 266 XP002019344 see the whole document ---	1-10, 12-22
A	BLOK L J ET AL: "ISOLATION OF cDNAs THAT ARE DIFFERENTIALLY EXPRESSED BETWEEN ANDROGEN-DEPENDENT AND ANDROGEN-INDEPENDENT PROSTATE CARCINOMA CELLS USING DIFFERENTIAL DISPLAY PCR" PROSTATE, vol. 26, no. 4, April 1995, pages 213-224, XP000611577 see the whole document ---	1-10, 12-22
A	ALEXEYEV ET AL.: "IMPROVED ANTIBIOTIC-RESISTANCE GENE CASSETTES AND OMEGA ELEMENTS FOR E.COLI VECTOR CONSTRUCTION AND IN VITRO DELETION/INSERTION MUTAGENESIS" GENE, vol. 160, 1995, pages 63-67, XP002076033 & DATABASE EMBL AC: U35129, 1995 "pBSL141" see abstract ---	1-10, 12-22
P,A	DATABASE EMBL AC: AA453562, 11 June 1997 HILLIER ET AL.: "HOMO SAPIENS cDNA CLONE 788180" XP002075910 see abstract -----	1-10, 12-22

# INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 98/03690

## Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1.  Claims Nos.:

because they relate to subject matter not required to be searched by this Authority, namely:

**Remark:** Although claims 6 and 7 are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.

2.  Claims Nos.:

because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3.  Claims Nos.:

because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see FURTHER INFORMATION sheet

1.  As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2.  As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3.  As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4.  No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-10, 12-22 (all partially)

### Remark on Protest

The additional search fees were accompanied by the applicant's protest.

No protest accompanied the payment of additional search fees.

**FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210**

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

**1. Claims: 1-10,12-22 (all partially)**

**Invention 1:**

Methods and diagnostic kits for detecting and monitoring prostate cancer comprising either a binding agent capable of binding to a polypeptide encoded by a DNA molecule with Seq. ID 2 or oligonucleotide primers specific for a DNA molecule with Seq. ID 2 as well as an monoclonal antibody binding to a prostate protein encoded by a DNA molecule with Seq. ID 2 used in a method for inhibiting development of prostate cancer.

**2. Claims: 1-10,12-22 (all partially)**

**Inventions 2-130:**

Methods and diagnostic kits for detecting and monitoring prostate cancer comprising either a binding agent capable of binding to a polypeptide encoded by a DNA molecule with Seq. ID 3 or oligonucleotide primers specific for a DNA molecule with Seq. ID 3 as well as an monoclonal antibody binding to a prostate protein encoded by a DNA molecule with Seq. ID 3 used in a method for inhibiting development of prostate cancer.

...ibidem for Seq. ID 8-29,  
41-45,47-52,54-65,70,73,74,79,81,87,90,92,93,97,103,104,107,1  
15-160,171,181,188,191,193,194,198,203,204,207,209-211,220,22  
2-224.

**3. Claims: 1-4,8,9,11-22 (all partially)**

**Inventions 131-215:**

Methods and diagnostic kits for detecting and monitoring prostate cancer comprising either a binding agent capable of binding to a polypeptide encoded by a DNA molecule with Seq. ID 5 or oligonucleotide primers specific for a DNA molecule with Seq. ID 5 as well as an monoclonal antibody binding to a prostate protein encoded by a DNA molecule with Seq. ID 5 used in a method for inhibiting development of prostate cancer.

...ibidem for each of Seq. ID  
6,7,30-40,46,53,66-69,71,72,75-78,80,82-86,88,89,91,94-96,98-  
102,105,106,161-170,179,180,182-187,189,190,192,195-197,198-2  
02,205,206,208,212-219.

**INTERNATIONAL SEARCH REPORT**

Information on patent family members

International Application No

PCT/JS 98/03690

Patent document cited in search report	Publication date	Patent family member(s)			Publication date
WO 9621671	A 18-07-1996	AU 4751196	A	31-07-1996	
		CA 2209941	A	18-07-1996	
		EP 0804458	A	05-11-1997	
WO 9314775	A 05-08-1993	CA 2106487	A	01-08-1993	
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		JP 8506005	T	02-07-1996	
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